Title: DNA Molecules and Polypeptides of *Pseudomonas syringae* Hrp Pathogenicity Island and Their Uses

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DNA Molecules and Polypeptides of *Pseudomonas syringae* Hrp Pathogenicity Island and Their Uses

This application claims benefit of U.S. Provisional Patent Application Serial Nos. 60/194,160, filed April 3, 2000, 60/224,604, filed August 11, 2000, and 60/249,548, filed November 17, 2000, which are hereby incorporated by reference in their entirety.

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Field of the Invention

The present invention relates to isolated DNA molecules corresponding to the open reading frames in the conserved effector loci and exchangeable effector loci of the *Pseudomonas syringae*, the isolated proteins encoded thereby, and their various uses.

Background of the Invention

The plant pathogenic bacterium *Pseudomonas syringae* is noted for its diverse and host-specific interactions with plants (Hirano and Upper, 1990). A specific strain may be assigned to one of at least 40 pathovars based on its host range among different plant species and then further assigned to a race based on differential interactions among cultivars of the host. In host plants the bacteria typically grow to high population levels in leaf intercellular spaces and then produce necrotic lesions. In nonhost plants or in host plants with race-specific resistance, the bacteria elicit the hypersensitive response (HR), a rapid, defense-associated programmed death of plant cells in contact with the pathogen (Alfano and Collmer, 1997). The ability to produce either of these reactions in plants appears to be directed by *hrp* (HR and pathogenicity) and *hrc* (HR and conserved) genes that encode a type III protein secretion pathway and by *avr* (avirulence) and *hop* (Hrp-dependent outer protein) genes that encode effector proteins injected into plant cells by the pathway (Alfano and Collmer, 1997). These effectors may also betray the parasite to the HR-triggering

R-gene surveillance system of potential hosts (hence the *avr* designation), and plant breeding for resistance based on such gene-for-gene (*avr-R*) interactions may produce complex combinations of races and differential cultivars (Keen, 1990). *hrp/hrc* genes are probably universal among necrosis-causing gram-negative plant pathogens, and they have been sequenced in *P. syringae* pv. syringae (*Psy*) 61, *Erwinia amylovora* Ea321, *Xanthomonas campestris* pv. vesicatoria (*Xcv*) 85-10, and *Ralstonia solanacearum* GMI1000 (Alfano and Collmer, 1997). Based on their distinct gene arrangements and regulatory components, the *hrp/hrc* gene clusters of these four bacteria can be divided into two groups: I (*Pseudomonas* and *Erwinia*) and II (*Xanthomonas* and *Ralstonia*). The discrepancy between the distribution of these groups and the phylogeny of the bacteria provides some evidence that *hrp/hrc* gene clusters have been horizontally acquired and, therefore, may represent pathogenicity islands (Pais) (Alfano and Collmer, 1997).

Pais have been defined as gene clusters that (i) include many virulence genes, (ii) are selectively present in pathogenic strains, (iii) have different G+C content compared to host bacteria DNA, (iv) occupy large chromosomal regions, (v) are often flanked by direct repeats, (vi) are bordered by tRNA genes and/or cryptic mobile genetic elements, and (vii) are unstable (Hacker et al., 1997). Some Pais have inserted into different genomic locations in the same species (Wieler et al., 1997). Others reveal a mosaic structure indicative of multiple horizontal acquisitions (Hensel et al., 1999). Genes encoding type III secretion systems are present in Pais in animal pathogenic *Salmonella* spp. and *Pseudomonas aeruginosa* and on large plasmids in *Yersinia* and *Shigella* spp. Genes encoding effectors secreted by the pathway in these organisms are commonly linked to the pathway genes (Hueck, 1998), although a noteworthy exception is *sopE*, which is carried by a temperate phage without apparent linkage to SPI1 in certain isolates of *S. typhimurium* (Mirold et al., 1999). Three *avr/hop* genes have already been shown to be linked to the *hrp/hrc* cluster in *P.* syringae: *avrE* and several other Hrp-regulated transcriptional units are linked to the *hrpR* border of the *hrp* cluster in *P. syringae* pv tomato (*Pto*) DC3000 (Lorang and Keen, 1995); *avrPphE* is adjacent to *hrpY* (*hrpK*) in *Pseudomonas phaseolicola* (*Pph*) 1302A (Mansfield et al., 1994); and *hopPsyA* (*hrmA*) is adjacent to *hrpK* in *Psy* 61 (Heu and Hutcheson, 1993). Other *Pseudomonas avr* genes are located elsewhere in

the genome or on plasmids (Leach and White, 1996), including a plasmid-borne group of *avr* genes described as a Pai in *Pph* 1449B (Jackson et al., 1999).

Because Avr, Hop, Hrp, and Hrc proteins represent promising therapeutic treatments in both plants and animals, it would be desirable to identify other proteins encoded by the Pai's in pathogenic bacteria and identify uses for those proteins.

The present invention overcomes these deficiencies in the art.

Summary of the Invention

One aspect of the present invention relates to isolated nucleic acid molecules (i) encoding proteins or polypeptides of *Pseudomonas* Conserved Effector Loci ("CEL") and Exchangeable Effector Loci ("EEL") genomic regions, (ii) nucleic acid molecules which hybridize thereto under stringent conditions, or (iii) nucleic acid molecules that include a nucleotide sequence which is complementary to the nucleic acid molecules of (i) and (ii). Expression vectors, host cells, and transgenic plants which include the DNA molecules of the present invention are also disclosed. Methods of making such host cells and transgenic plant are disclosed.

A further aspect of the present invention relates to isolated proteins or polypeptides encoded by the nucleic acid molecules of the present invention. Compositions which contain the proteins are also disclosed.

Yet another aspect of the present invention relates to methods of imparting disease resistance to a plant. According to one approach, this method is carried out by transforming a plant cell with a heterologous DNA molecule of the present invention and regenerating a transgenic plant from the transformed plant cell, wherein the transgenic plant expresses the heterologous DNA molecule under conditions effective to impart disease resistance. According to another approach, this method is carried out by treating a plant with a protein or polypeptide of the present invention under conditions effective to impart disease resistance to the treated plant.

A still further aspect of the present invention relates to a method of making a plant hypersusceptible to colonization by nonpathogenic bacteria. According to one approach, this method is carried out by transforming a plant cell with a heterologous DNA molecule of the present invention and regenerating a

transgenic plant from the transformed plant cell, wherein the transgenic plant expresses the heterologous DNA molecule under conditions effective to render the transgenic plant hypersusceptible to colonization by nonpathogenic bacteria. According to an alternative approach, this method is carried out by treating a plant with a protein or polypeptide of the present invention under conditions effective to render the treated plant susceptible to colonization by nonpathogenic bacteria.

Another aspect of the present invention relates to a method of causing eukaryotic cell death by introducing into a eukaryotic cell a cytotoxic *Pseudomonas* protein, where the introducing is performed under conditions effective to cause cell death.

A further aspect of the present invention relates to a method of treating a cancerous condition by introducing a cytotoxic *Pseudomonas* protein into cancer cells of a patient under conditions effective to cause death of cancer cells, thereby treating the cancerous condition.

The benefits of the present invention result from three factors. First, there is substantial and growing evidence that phytopathogen effector proteins have evolved to elicit exquisite changes in eukaryote metabolism at extremely low levels, and at least some of these activities are potentially relevant to mammals and other organisms in addition to plants. For example, ORF5 in the *Psy* B728a EEL is similar to *Xanthomonas campestris* pv. *vesicatoria* AvrBsT, a phytopathogen protein that appears to have the same active site as its animal pathogen homolog YopJ, which inhibits mammalian MAPKK defense signaling (Orth et al., 2000). Second, the *P. syringae* CEL and EEL regions are enriched in effector protein genes, which makes these regions fertile targets for effector genc bioprospecting. Third, rapidly developing technologies for delivering genes and proteins into plant and animal cells improve the efficacy of protein-based therapies.

Brief Description of the Drawings

Figure 1 is a diagram illustrating the conserved arrangement of *hrp/hrc* genes within the Hrp Pais of *Psy* 61, *Psy* B728a, and *Pto* DC3000. Regions sequenced in B728a and DC3000 are indicated by lines beneath the strain 61 sequence. Known regulatory genes are shaded. Arrows indicate the direction of

transcription, with small boxes denoting the presence of a Hrp box. The triangle denotes the 3.6-kb insert with phage genes in the B728a *hrp/hrc* region.

Figures 2A-C show the EEL of *Pto* DC3000, *Psy* B728a, and *Psy* 61, the *tgt-queA*-tRNA^{Leu} locus in *P. aeruginosa* (*Pa*), and EEL border sequences. Figure 2A is a diagram of the EELs of three *P. syringae* strains shown aligned by their *hrpK* sequences and are compared with the *tgt-queA*-tRNA^{Leu} locus in *Pa* PA01. Arrows indicate the direction of transcription, with small boxes denoting the presence of a Hrp box. Shaded regions are conserved, striped regions denote mobile genetic elements, and open boxes denote genes that are completely dissimilar from each other. Figure 2B is an alignment of the sequences of the DC3000 (DC) (SEQ. ID. No. 85), B728a (B7) (SEQ. ID. No. 86), and 61 (SEQ. ID. No. 87) EELs at the border with tRNA^{Leu}, with conserved nucleotides shown in upper case. Figure 2C is an alignment of the sequences of the DC3000 (DC) (SEQ. ID. No. 88), B728a (B7) (SEQ. ID. No. 89), and 61 (SEQ. ID. No. 90) EELs at the border with *hrpK*, with conserved nucleotides shown in upper case.

Figure 3 is a diagram illustrating the Hrp Pai CEL of *P. syringae*. The *Pto* DC3000 CEL is shown with the corresponding fragments of *Psy* B728a that were sequenced aligned below. The nucleotide identity of the sequenced fragments in coding regions ranged from 72% to 83%. Arrows indicate the direction of transcription, with small boxes denoting the presence of a Hrp box.

Figures 4A-E illustrate the plant interaction phenotypes of *Pto* mutants carrying deletions of the EEL (CUCPB5110) and CEL (CUCPB5115). Figure 14A is a graph illustrating growth in tomato of DC3000 and CUCPB5110 (mean and SD). Figure 14B is a graph illustrating growth in tomato of DC3000, CUCPB5115, and CUCPB5115(pCPP3016) (mean and SD). Figure 14C is an image showing HR collapse in tobacco leaf tissue 24 h after infiltration with 10^7 cfu/ml of DC3000 and CUCPB5115. Figure 14D is an image showing the absence of disease symptoms in tomato leaf 4 days after inoculation with 10^4 cfu/ml of CUCPB5115. Figure 14E is an image showing disease symptoms typical of wild-type in tomato leaf 4 days after inoculation with 10^4 cfu/ml of CUCPB5115(pCPP3016).

Figure 5 is an image of the immunoblot analysis showing AvrPto secretion by *Pto* DC3000 derivatives with deletions affecting the three major regions

of the Hrp Pai. Bacteria were grown in Hrp-inducing minimal medium at pH 5.5 and 22°C to an OD_{600} of 0.35 and then separated into cell-bound (C) and supernatant (S) fractions by centrifugation. Proteins were then resolved by SDS-PAGE, blotted, and immunostained with antibodies against AvrPto and β-lactamase as described (Manceau and Harvais, 1997), except that supernatant fractions were concentrated 3-fold relative to cell-bound fractions before loading. *Pto* DC3000, CUCPB5115 (CEL deletion), CUCPB5114 (*hrp/hrc* deletion), and CUCPB5110 (EEL deletion) all carried pCPP2318, which expresses β-lactamase without a signal peptide as a cytoplasmic marker.

Figures 6A-B illustrate, enlarged as compared to Figure 1, the organization of the *shcA* and *hopPsyA* operon in the EEL of the Hrp Pai of *Psy* 61. In Figure 6A, the *shcA* and *hopPsyA* are depicted as white boxes. At the border of the Hrp Pai are the $tRNA^{Leu}$ and *queA* genes depicted as gray boxes. A 5' truncated *hrpK* gene is represented as a hatched box. The arrows indicate the predicted direction of transcription and the black box denotes the presence of a putative HrpL-dependent promoter upstream of *shcA*. Figure 6B illustrates schematically the construction of the deletion mutation in the *shcA* ORF marker-exchanged into *Psy* 61. Black bars depict regions that were amplified along with added restriction enzyme sites and each are aligned with the corresponding DNA region represented in Figure 6A. The striped box depicts the *nptII* cassette that lacks transcriptional and translational terminators used in making the functionally nonpolar *shcA Psy* 61 mutant. *Eco*RI, E; *Eco*RV, V; *Xba*I, X; and *Xho*I, Xh.

Figure 7 is an image of an immunoblot showing that *shcA* encodes a protein product. pLV9 is a derivative of pFLAG-CTC in which the *shcA* ORF is cloned and fused to the FLAG epitope and translation is directed by a vector ribosome binding site (RBS). pLV26 contains an amplified product containing the *shcA* coding region and its native RBS site. Cultures of *E. coli* DH5α carrying either pFLAG-CTC (Control), pLV9, or pLV26 were grown to an OD_{600} of 0.8 and then 100 µl aliquots were taken, centrifuged, resuspended in SDS-PAGE buffer, and then subjected to SDS-PAGE and immunoblot analysis with anti-FLAG antibodies and secondary antibodies conjugated with alkaline phosphatase.

Figure 8 is an image of an immunoblot showing that *Psy* 61 *shcA* mutant UNLV102 does not secrete HopPsyA and *shcA* provided *in trans* complements this defect. *Psy* 61 cultures were grown at 22°C in *hrp*-derepressing medium and separated into cell-bound (C) and supernatant fractions (S). The cell-bound fractions were concentrated 13.4-fold and the supernatant fractions were concentrated 100-fold relative to the initial culture volumes. The samples were subjected to SDS-PAGE and immunoblot analysis, and HopPsyA and β-lactamase (Bla) were detected with either anti-HopPsyA or anti-β-lactamase antibodies followed by secondary antibodies conjugated to alkaline phosphatase as described in the experimental procedures. The image of the immunoblot was captured using the Bio-Rad Gel Doc 2000 UV fluorescent gel documentation system with the accompanying Quantity 1 software.

Figure 9 is an image of an immunoblot showing that *shcA* is required for the type III secretion of HopPsyA, but not secretion of HrpZ. *P. fluorescens* 55 cultures were grown in *hrp*-derepressing medium and separated into cell-bound (C) and supernatant (S) fractions. The cell-bound fractions were concentrated 13.4-fold and the supernatant fractions were concentrated 100-fold relative to the initial culture volumes. The samples were subjected to SDS-PAGE and immunoblot analysis, and HopPsyA and HrpZ were detected with either anti-HopPsyA or anti-HrpZ antibodies followed by secondary antibodies conjugated to alkaline phosphatase as described in experimental procedures. The image of the immunoblot was captured using the Bio-Rad Gel Doc 2000 UV fluorescent gel documentation system with the accompanying Quantity 1 software.

Figure 10 is a series of four images of tobacco leaves showing that *P. fluorescens* 55 carrying a pHIR11 derivative with a functionally nonpolar *shcA* mutation is impaired in its ability to translocate HopPsyA into plant cells. *P. fluorescens* 55 cultures were grown overnight in King's B and suspended in 5 mM MES pH 5.6 to an OD_{600} of 1.0, and infiltrated into tobacco leaf panels. Because the pHIR11-induced HR is due to the translocation of HopPsyA inside plant cells, a reduced HR indicates that HopPsyA is not delivered well enough to induce a typical HR. The leaf panels were photographed with incident light 24 hours later.

Figure 11 is an image of an immunoblot showing that ShcA binds to HopPsyA. Soluble protein samples from sonicated cultures (Sonicate) of *Psy* 61 *shcA* mutant UNLV102 carrying pLN1 (HopPsyA) or pLN2 (ShcA-FLAG, HopPsyA) were mixed with anti-FLAG M2 affinity gel (Gel). Tbe gel was washed (Wasb) with TBS buffer, mixed with SDS-PAGE buffer, and subjected to SDS-PAGE and immunoblot analysis along with the sonicate and wash samples. HopPsyA and ShcA-FLAG were detected with anti-HopPsyA or anti-FLAG antibodies followed by secondary antibodies conjugated to alkalinc phosphatase as described in experimental procedures.

Figure 12 is a diagram illustrating the spindle checkpoint in *S. cerevisiae*. The spindle checkpoint is activated by a signal emitted from the kinetochores when there are abnormalities with the microtubules. This signal is somehow received by the spindle checkpoint components, which respond in a variety of ways. Mad2 is thought to bind to Cdc20 at the APC inhibiting its ubiquitin ligase activity. In the absence of Mad2 (and presumably damage to the spindle), the APC is active and it marks Pds1 and other inhibitors of anaphase for degradation via the ubiquitin proteolysis pathway; anaphase ensues.

Figures 13A-B illustrate the effects of transgenically expressed HopPsyA on *Nicotiana tabacum* cv. Xanthi, *Nicotiana benthamiana*, and *Arabidopsis thaliana*. Figure 13A shows *N. tabacum* cv. Xanthi and *N. benthamiana* leaves infiltrated with *Agrobacterium tumefaciens* GV3101 with or without pTA7002::*hopPsyA*. Figure 13B illustrates *Arabidopsis thaliana* Col-1 infiltrated with *A. tumefaciens* +/- pTA7002::*hopPsyA*. For all plants shown in Figures 13A-B, 48 h after *Agrobacterium* infiltration, plants were sprayed with the glucocorticoid dexamethasone (DEX). Images were collected 24 h after DEX treatment. *A.t.* = *Agrobacterium tumefaciens*; pA = pTA7002::*hopPsyA*.

Figure 14 is an image of an SDS-PAGE which shows the distribution of HopPsyA and β-lactamase in cultures of *Psy* 61 (pCPP2318) or a *hrp* mutant, *Psy* 61-2089 (pCPP2318). Bacterial cultures were grown at 22°C in *hrp*-depressing medium and separated into cell-bound (C) and supernatant fractions (S). The cell-bound fractions were concentrated 13.4 fold, and the supernatant fractions were concentrated 100 fold relative to initial culture volumes. The samples were subjected

to SDS-PAGE and immunoblot analysis and HopPsyA and β-lactamase were detected with either anti- HopPsyA or anti-β-lactamase antibodies followed by secondary antibodies conjugated to alkaline phosphatase. *Pss* wild-type = *Pseudomonas syringae* pv. syringae 61 (pCPP2318); *Pss hrcC* = *Pseudomonas syringae* pv. syringae 61-2089 (pCPP2318).

Figure 15 is a graph illustrating the ability of wild-type *Pseudomonas syringae* pv. syringae and a *hopPsyA* mutant to multiply in bean leaves. Values represent the average plate counts from crushed plant leaves of two independent inoculations. Wild-type (●), *Pseudomonas syringae* pv. syringae 61; *hopPsyA* mutant (○), *Pseudomonas syringae* pv. syringae 61-2070.

Figures 16A-B illustrate the interaction of HopPsyA and Mad2 in a yeast two-hybrid assay. Figure 16A illustrates cultures of yeast EGY48 strains containing either pLV24 (pEG202::*'hopPsyA*) and pJG4-5 (fish-vector), pLV24 and pLV116 (pJG4-5::*mad2*), or pEG202 (bait vector) and pLV116 on medium containing 5-bromo-4-chloro-3-indolyl-β-D-galactopyranoside (Xgal) to check for β-galactosidase activity with either glucose (Glc) or galactose (Gal). β-galactosidase activity was indicated only in the presence of both HopPsyA and Mad2. Figure 16B illustrates cultures of the same yeast strains on minimal medium leucine dropout plates with either Glc or Gal sugars. 1 = EGY48 (pLV24, pJG4-5); 2 = EGY48 (pLV24, pLV116); 3 = EGY48 (pEG202, pLV116).

Dctailed Description of the Invention

A DNA molecule which contains the CEL of *Pseudomonas syringae* pv. tomato DC3000 has a nucleotide sequence (SEQ. ID. No. 1) as follows:

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ggtaccgggc tctgtgacgc agagcgtcac gcaaggcatt ccactggagc gtgaggaacg 60
ataatcctga cgacaactat cgtgcgacgc tccgcgtcgg catgccgttc tggacgctct 120
gcgtcctgtc ttgagaggtg cgccaagcgc aaagcacggt aagtatcagg gaggggtgta 180
taggagggtt gcaaggcggg aggtgttcat atcaaggcag tgttcatgaa cccgtcttgc 240
ctgggctcat gaacacgttc ggcttacgcg gtcagtgcat ttcctcgctc aaatggtcca 300
gccctgccag catcaactca tgccggtgga tgtcgtccag gctggcgtag gaacccggtt 360
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gattgaaacg ctctgactcc ataaaacgtc gttgcagtgc atcacgcagt tgatcgggac 480
gcaacgcgcg gccttctatg tgcaaggcga tcccccaatc atggtgttcg cgccgactga 540
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atcgt                                                          30365
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Several undefined nucleotides exist in SEQ. ID. No. 1, however these appear to be present in intergenic regions. The CEL of *Pseudomonas syringae* pv. tomato DC3000 contains a number of open reading frames (ORFs). Two of the products encoded by the CEL are HrpW and AvrE, both of which are known. An additional 10 products are produced by ORF1-10, respectively, as shown in Figure 3. The nucleotide sequences for a number of these ORFs and their encoded protein or polypeptide products are provided below.

The DNA molecule of *ORF3* from the *Pseudomonas syringae* pv. tomato DC3000 CEL has a nucleotide sequence (SEQ. ID. No. 2) as follows:

```
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cggctgaatg tcgcggctcg acacacacag cttttgcagg ccttcaaggc tgagcatggg 240
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ctgcacgctg acaggcaggc gctggtcgac gccaaaacca ccctggtagg tttgcacgcc 780
gatttcgtca agtcgccgga ggccaagcgc cttgcttcgg tcgccgcaca tacgcaactg 840
gacaacgtcg tcagcgatct cgtcactgcc cgtaacacgg tgggtggctg gaaaggtgca 900
gggccgattg tcgcggctgc ggttccgcag ttcttgtctt caatgacaca cttgggttat 960
gtgcgtttgt ccaccagcga caagctgcga gacacgattc ccgagaccag cagcgacgcc 1020
aacatgctca aggcttcgat aatcgggatg gtggcgggca ttgctcacga gacggtcaac 1080
agcgtggtca agccgatgtt tcaggccgcc ttgcagaaga ctggcctcaa cgaacgcctg 1140
aacatggtgc caatgaaggc tgtggatacc aatacggtta ttcctgaccc cttcgagctg 1200
aaaagcgaac acggtgagct ggtcaaaaaa acgcccgagg aagtcgctca ggacaaggcg 1260
ttcgtgaaaa gtgaacgcgc gctgctgaac cagaagaagg ttcagggttc gtccacccat 1320
ccggtaggtg agctgatggc ttacagtgcc ttcggtggtt ctcaggctgt gcgccagatg 1380
ctcaacgatg ttcaccagat caatgggcag acgctgagtg caagagctct ggcatccggt 1440
tttggcgggg cggtgtctgc cagttcgcaa acgctgctgc aattgaagtc gaattatgtc 1500
gacccgcaag ggcgcaaaat tccggtattt accccggacc gcgccgagag cgatctgaaa 1560
aaggacctgc tcaaaggtat ggacctgcgc gagccgtcgg tacgcaccac gttctacagc 1620
aaggctcttt cgggtattca gagttctgca ctgacctcgg cactgccgcc tgtgaccgct 1680
caggctgaag gcgcaagtgg cacgctcagt gcgggggcta ttttgcgcaa catggccctg 1740
gcagcgacgg gttcggtgtc ctatctgtcc acgttgtaca ccaaccagtc ggttaccgca 1800
gaagccaagg cgttgaaagc ggcaggcatg ggcggtgcaa cacctatgct ggaccgtacc 1860
gagacgcttt ga                                                    1872
```

The protein or polypeptide encoded by *Pto* DC3000 CEL *ORF3* has an amino acid sequence (SEQ. ID. No. 3) as follows:

```
Met Ile Ser Ser Arg Ile Gly Gly Ala Gly Gly Val Lys Leu Ser Arg
 1               5                  10                  15

Val Asn Gln Gln His Asp Thr Val Pro Ala Gln Thr Ala His Pro Asn
            20                  25                  30

Ala Val Thr Ala Gly Met Asn Pro Pro Leu Thr Pro Asp Gln Ser Gly
        35                  40                  45

Ser His Ala Thr Glu Ser Ser Ser Ala Gly Ala Ala Arg Leu Asn Val
    50                  55                  60

Ala Ala Arg His Thr Gln Leu Leu Gln Ala Phe Lys Ala Glu His Gly
65                  70                  75                  80

Thr Ala Pro Val Ser Gly Ala Pro Met Ile Ser Ser Arg Ala Ala Leu
                85                  90                  95

Leu Ile Gly Ser Leu Leu Gln Ala Glu Pro Leu Pro Phe Glu Val Met
            100                 105                 110

Ala Glu Lys Leu Ser Pro Glu Arg Tyr Gln Leu Lys Gln Phe Gln Gly
        115                 120                 125

Ser Asp Leu Gln Gln Arg Leu Glu Lys Phe Ala Gln Pro Gly Gln Ile
    130                 135                 140

Pro Asp Lys Ala Glu Val Gly Gln Leu Ile Lys Gly Phe Ala Gln Ser
145                 150                 155                 160

Val Ala Asp Gln Leu Glu His Phe Gln Leu Met His Asp Ala Ser Pro
                165                 170                 175
```

```
Ala Thr Val Gly Gln His Ala Lys Ala Asp Lys Ala Thr Leu Ala Val
            180                 185                 190

Ser Gln Thr Ala Leu Gly Glu Tyr Ala Gly Arg Ala Ser Lys Ala Ile
        195                 200                 205

Gly Glu Gly Leu Ser Asn Ser Ile Ala Ser Leu Asp Glu His Ile Ser
    210                 215                 220

Ala Leu Asp Leu Thr Leu Gln Asp Ala Glu Gln Gly Asn Lys Glu Ser
225                 230                 235                 240

Leu His Ala Asp Arg Gln Ala Leu Val Asp Ala Lys Thr Thr Leu Val
                245                 250                 255

Gly Leu His Ala Asp Phe Val Lys Ser Pro Glu Ala Lys Arg Leu Ala
            260                 265                 270

Ser Val Ala Ala His Thr Gln Leu Asp Asn Val Val Ser Asp Leu Val
        275                 280                 285

Thr Ala Arg Asn Thr Val Gly Gly Trp Lys Gly Ala Gly Pro Ile Val
    290                 295                 300

Ala Ala Ala Val Pro Gln Phe Leu Ser Ser Met Thr His Leu Gly Tyr
305                 310                 315                 320

Val Arg Leu Ser Thr Ser Asp Lys Leu Arg Asp Thr Ile Pro Glu Thr
                325                 330                 335

Ser Ser Asp Ala Asn Met Leu Lys Ala Ser Ile Ile Gly Met Val Ala
            340                 345                 350

Gly Ile Ala His Glu Thr Val Asn Ser Val Val Lys Pro Met Phe Gln
        355                 360                 365

Ala Ala Leu Gln Lys Thr Gly Leu Asn Glu Arg Leu Asn Met Val Pro
    370                 375                 380

Met Lys Ala Val Asp Thr Asn Thr Val Ile Pro Asp Pro Phe Glu Leu
385                 390                 395                 400

Lys Ser Glu His Gly Glu Leu Val Lys Lys Thr Pro Glu Glu Val Ala
                405                 410                 415

Gln Asp Lys Ala Phe Val Lys Ser Glu Arg Ala Leu Leu Asn Gln Lys
            420                 425                 430

Lys Val Gln Gly Ser Ser Thr His Pro Val Gly Glu Leu Met Ala Tyr
        435                 440                 445

Ser Ala Phe Gly Gly Ser Gln Ala Val Arg Gln Met Leu Asn Asp Val
    450                 455                 460

His Gln Ile Asn Gly Gln Thr Leu Ser Ala Arg Ala Leu Ala Ser Gly
465                 470                 475                 480

Phe Gly Gly Ala Val Ser Ala Ser Ser Gln Thr Leu Leu Gln Leu Lys
                485                 490                 495

Ser Asn Tyr Val Asp Pro Gln Gly Arg Lys Ile Pro Val Phe Thr Pro
            500                 505                 510

Asp Arg Ala Glu Ser Asp Leu Lys Lys Asp Leu Leu Lys Gly Met Asp
        515                 520                 525
```

```
Leu Arg Glu Pro Ser Val Arg Thr Thr Phe Tyr Ser Lys Ala Leu Ser
    530                 535                 540

Gly Ile Gln Ser Ser Ala Leu Thr Ser Ala Leu Pro Pro Val Thr Ala
545                 550                 555                 560

Gln Ala Glu Gly Ala Ser Gly Thr Leu Ser Ala Gly Ala Ile Leu Arg
                565                 570                 575

Asn Met Ala Leu Ala Ala Thr Gly Ser Val Ser Tyr Leu Ser Thr Leu
            580                 585                 590

Tyr Thr Asn Gln Ser Val Thr Ala Glu Ala Lys Ala Leu Lys Ala Ala
        595                 600                 605

Gly Met Gly Gly Ala Thr Pro Met Leu Asp Arg Thr Glu Thr Leu
    610                 615                 620
```

The DNA molecule of *ORF4* from the *Pseudomonas syringae* pv. tomato DC3000 CEL has a nucleotide sequence (SEQ. ID. No. 4) as follows:

```
atgaccaaca atgaccagta ccacaccctt atcaacgaaa tctgcgcact cagcctgatt 60
tccacacctg aacgtttcta tgaatctgcc aatttcaaaa tcagcgaagt ggacttcacc 120
ctgcagtttc aggaccgcga cgaaggccgt gccgttctga tctacggtga catgggcgcg 180
ttgcccgcgc gcggccgtga gagcgcgttg ctggcgttga tggacatcaa ctttcacatg 240
ttcgcgggcg cccacagccc ggcatttttcc tttaatgcgc agaccggtcg tgtgctgctg 300
atgggctctg tggcccttga acgagcctct gccgaaggcg tgctgttgtt gatgaagtcg 360
ttttccgacc tggccaaaga gtggcgcgag catggattca tggggcaggc cacaactgca 420
ggctcctcga cggaccaacc tgttgcccca gcagccaaac gcgagagcct ttcggctcct 480
gggagattcc aatga                                                  495
```

The protein or polypeptide encoded by *Pto* DC3000 CEL *ORF4* has an amino acid sequence (SEQ. ID. No. 5) as follows:

```
Met Thr Asn Asn Asp Gln Tyr His Thr Leu Ile Asn Glu Ile Cys Ala
  1               5                  10                  15

Leu Ser Leu Ile Ser Thr Pro Glu Arg Phe Tyr Glu Ser Ala Asn Phe
            20                  25                  30

Lys Ile Ser Glu Val Asp Phe Thr Leu Gln Phe Gln Asp Arg Asp Glu
        35                  40                  45

Gly Arg Ala Val Leu Ile Tyr Gly Asp Met Gly Ala Leu Pro Ala Arg
    50                  55                  60

Gly Arg Glu Ser Ala Leu Leu Ala Leu Met Asp Ile Asn Phe His Met
65                  70                  75                  80

Phe Ala Gly Ala His Ser Pro Ala Phe Ser Phe Asn Ala Gln Thr Gly
                85                  90                  95

Arg Val Leu Leu Met Gly Ser Val Ala Leu Glu Arg Ala Ser Ala Glu
            100                 105                 110

Gly Val Leu Leu Leu Met Lys Ser Phe Ser Asp Leu Ala Lys Glu Trp
        115                 120                 125
```

```
Arg Glu His Gly Phe Met Gly Gln Ala Thr Thr Ala Gly Ser Ser Thr
    130                 135                 140

Asp Gln Pro Val Ala Pro Ala Ala Lys Arg Glu Ser Leu Ser Ala Pro
145                 150                 155                 160

Gly Arg Phe Gln
```

The DNA molecule of *ORF5* from the *Pseudomonas syringae* pv. tomato DC3000 CEL has a nucleotide sequence (SEQ. ID. No. 6) as follows:

```
atgcacatca accgacgcgt ccaacaaccg cctgtgactg cgacggatag ctttcggaca 60
gcgtccgacg cgtctcttgc ctccagctct gtgcgatctg tcagctccga tcagcaacgc 120
gagataaatg cgattgccga ttacctgaca gatcatgtgt tcgctgcgca taaactgccg 180
ccggccgatt cggctgatgg ccaagctgca gttgacgtac acaatgcgca gatcactgcg 240
ctgatcgaga cgcgcgccag ccgcctgcac ttcgaagggg aaaccccggc aaccatcgcc 300
gacaccttcg ccaaggcgga aaagctcgac cgattggcga cgactacatc aggcgcgttg 360
cgggcgacgc cctttgccat ggcctcgttg cttcagtaca tgcagcctgc gatcaacaag 420
ggcgattggc tgccggctcc gctcaaaccg ctgaccccgc tcatttccgg agcgctgtcg 480
ggcgccatgg accaggtggg caccaagatg atggaccgcg cgacgggtga tctgcattac 540
ctgagcgcct cgccggacag gctccacgat gcgatggccg cttcggtgaa gcgccactcg 600
ccaagccttg ctcgacaggt tctggacacg ggggttgcgg ttcagacgta ctcggcgcgc 660
aacgccgtac gtaccgtatt ggctccggca ctggcgtcca gacccgccgt gcagggtgct 720
gtggaccttg gtgtatcgat ggcgggtggt ctggctgcca acgcaggctt tggcaaccgc 780
ctgctcagtg tgcagtcgcg tgatcaccag cgtggcggtg cattagtgct cggtttgaag 840
gataaagagc ccaaggctca actgagcgaa gaaaacgact ggctcgaggc ttataaagca 900
atcaaatcgg ccagctactc gggtgcggcg ctcaacgctg gcaagcggat ggccggtctg 960
ccactggata tggcgaccga cgcaatgggt gcggtaagaa gcctggtgtc agcgtccagc 1020
ctgacccaaa acggtctggc cctggcgggt ggctttgcag gggtaggcaa gttgcaggag 1080
atggcgacga aaaatatcac cgacccggcg accaaggccg cggtcagtca gttgaccaac 1140
ctggcaggtt cggcagccgt tttcgcaggc tggaccacgg ccgcgctgac aaccgatccc 1200
gcggtgaaaa aagccgagtc gttcatacag gacacggtga aatcgactgc atccagtacc 1260
acaggctacg tagccgacca gaccgtcaaa ctggcgaaga ccgtcaaaga catgggcggg 1320
gaggcgatca cccataccgg cgccagcttg cgcaatacgg tcaataacct gcgtcaacgc 1380
ccggctcgtg aagctgatat agaagagggg ggcacggcgg cttctccaag tgaaataccg 1440
tttcggccta tgcggtcgta a                                          1461
```

The protein or polypeptide encoded by *Pto* DC3000 CEL *ORF5*, now known as HopPtoA, has an amino acid sequence (SEQ. ID. No. 7) as follows:

```
Met His Ile Asn Arg Arg Val Gln Gln Pro Pro Val Thr Ala Thr Asp
 1               5                  10                  15

Ser Phe Arg Thr Ala Ser Asp Ala Ser Leu Ala Ser Ser Ser Val Arg
            20                  25                  30

Ser Val Ser Ser Asp Gln Gln Arg Glu Ile Asn Ala Ile Ala Asp Tyr
        35                  40                  45

Leu Thr Asp His Val Phe Ala Ala His Lys Leu Pro Pro Ala Asp Ser
    50                  55                  60

Ala Asp Gly Gln Ala Ala Val Asp Val His Asn Ala Gln Ile Thr Ala
65                  70                  75                  80
```

Leu Ile Glu Thr Arg Ala Ser Arg Leu His Phe Glu Gly Glu Thr Pro
85 90 95

Ala Thr Ile Ala Asp Thr Phe Ala Lys Ala Glu Lys Leu Asp Arg Leu
100 105 110

Ala Thr Thr Thr Ser Gly Ala Leu Arg Ala Thr Pro Phe Ala Met Ala
115 120 125

Ser Leu Leu Gln Tyr Met Gln Pro Ala Ile Asn Lys Gly Asp Trp Leu
130 135 140

Pro Ala Pro Leu Lys Pro Leu Thr Pro Leu Ile Ser Gly Ala Leu Ser
145 150 155 160

Gly Ala Met Asp Gln Val Gly Thr Lys Met Met Asp Arg Ala Thr Gly
165 170 175

Asp Leu His Tyr Leu Ser Ala Ser Pro Asp Arg Leu His Asp Ala Met
180 185 190

Ala Ala Ser Val Lys Arg His Ser Pro Ser Leu Ala Arg Gln Val Leu
195 200 205

Asp Thr Gly Val Ala Val Gln Thr Tyr Ser Ala Arg Asn Ala Val Arg
210 215 220

Thr Val Leu Ala Pro Ala Leu Ala Ser Arg Pro Ala Val Gln Gly Ala
225 230 235 240

Val Asp Leu Gly Val Ser Met Ala Gly Gly Leu Ala Ala Asn Ala Gly
245 250 255

Phe Gly Asn Arg Leu Leu Ser Val Gln Ser Arg Asp His Gln Arg Gly
260 265 270

Gly Ala Leu Val Leu Gly Leu Lys Asp Lys Glu Pro Lys Ala Gln Leu
275 280 285

Ser Glu Glu Asn Asp Trp Leu Glu Ala Tyr Lys Ala Ile Lys Ser Ala
290 295 300

Ser Tyr Ser Gly Ala Ala Leu Asn Ala Gly Lys Arg Met Ala Gly Leu
305 310 315 320

Pro Leu Asp Met Ala Thr Asp Ala Met Gly Ala Val Arg Ser Leu Val
325 330 335

Ser Ala Ser Ser Leu Thr Gln Asn Gly Leu Ala Leu Ala Gly Gly Phe
340 345 350

Ala Gly Val Gly Lys Leu Gln Glu Met Ala Thr Lys Asn Ile Thr Asp
355 360 365

Pro Ala Thr Lys Ala Ala Val Ser Gln Leu Thr Asn Leu Ala Gly Ser
370 375 380

Ala Ala Val Phe Ala Gly Trp Thr Thr Ala Ala Leu Thr Thr Asp Pro
385 390 395 400

Ala Val Lys Lys Ala Glu Ser Phe Ile Gln Asp Thr Val Lys Ser Thr
405 410 415

Ala Ser Ser Thr Thr Gly Tyr Val Ala Asp Gln Thr Val Lys Leu Ala
420 425 430

```
Lys Thr Val Lys Asp Met Gly Gly Glu Ala Ile Thr His Thr Gly Ala
        435                 440                 445

Ser Leu Arg Asn Thr Val Asn Asn Leu Arg Gln Arg Pro Ala Arg Glu
    450                 455                 460

Ala Asp Ile Glu Glu Gly Gly Thr Ala Ala Ser Pro Ser Glu Ile Pro
465                 470                 475                 480

Phe Arg Pro Met Arg Ser
                485
```

The DNA molecule of *ORF6* from the *Pseudomonas syringae* pv. tomato DC3000 CEL has a nucleotide sequence (SEQ. ID. No. 8) as follows:

```
atgtctggtc ctttcgagaa aaaatggcgg tgtttcaccc gaaccgtgac ctacgttggc 60
tggtcgctgt tctggcttct gctctgggac gtggccgtca ccgtggacgt catgctgata 120
gaaggcaaag gcatcgactt ccccctgatg ccccтcacgt tgctttgctc ggcactgatc 180
gtgctgatca gctttcgcaa ctcgagtgcc tataaccgtt ggtgggaagc gcgcaccttg 240
tggggcgcaa tggtcaacac ttcacgcagt tttggccggc aggtactgac gctgatcgat 300
ggcgaacggg atgacctcaa caaccctgtc aaagccatac tctttcaacg tcatgtggct 360
tacttgcgtg ccctgcgcgc gcacctcaaa ggcgacgtca aaacagcaaa actcgacggg 420
ttactgtcgc ccgacgagat tcagcgcgcc agccagagca acaacttccc caatgacatc 480
ctcaatggct ctgctgcggt tatctcgcaa gcctttgccg ccggccagtt cgacagcatc 540
cgtctgaccc gcctggaatc gaccatggtc gatctgtcca actgtcaggg cggcatggag 600
cgcatcgcca acacgccact gccctacccc tacgtttatt tcccacggct gttcagcacg 660
ctgttctgca tcctgatgcc gctgagcatg gtcaccaccc tgggctggtt caccccggcg 720
atctccacgg tggtaggctg catgctgctg gcaatggacc gcatcggtac agacctgcaa 780
gccccgttcg gcaacagtca gcaccggatc cgcatggaag acctgtgcaa caccatcgaa 840
aagaacctgc aatcgatgtt ctcttcgcca gagaggcagc cgctgctggc tgacctgaaa 900
agccccgtac cgtggcgcgt ggccaacgca tcaattggcg gtctgagcag gcagaaaaac 960
aggttagggg aaggcgcgag gcttatcgca agtgaaagtc tgctctgggc accatttcgc 1020
tcagttgcag acgttgctcc gtgccacgcc agtgcgtacc tacgtcgcgc ttga       1074
```

The protein or polypeptide encoded by *Pto* DC3000 CEL *ORF6* has an amino acid sequence (SEQ. ID. No. 9) as follows:

```
Met Ser Gly Pro Phe Glu Lys Lys Trp Arg Cys Phe Thr Arg Thr Val
  1               5                  10                  15

Thr Tyr Val Gly Trp Ser Leu Phe Trp Leu Leu Leu Trp Asp Val Ala
             20                  25                  30

Val Thr Val Asp Val Met Leu Ile Glu Gly Lys Gly Ile Asp Phe Pro
         35                  40                  45

Leu Met Pro Leu Thr Leu Leu Cys Ser Ala Leu Ile Val Leu Ile Ser
     50                  55                  60

Phe Arg Asn Ser Ser Ala Tyr Asn Arg Trp Trp Glu Ala Arg Thr Leu
 65                  70                  75                  80

Trp Gly Ala Met Val Asn Thr Ser Arg Ser Phe Gly Arg Gln Val Leu
                 85                  90                  95

Thr Leu Ile Asp Gly Glu Arg Asp Asp Leu Asn Asn Pro Val Lys Ala
            100                 105                 110
```

```
Ile Leu Phe Gln Arg His Val Ala Tyr Leu Arg Ala Leu Arg Ala His
        115                 120                 125

Leu Lys Gly Asp Val Lys Thr Ala Lys Leu Asp Gly Leu Leu Ser Pro
    130                 135                 140

Asp Glu Ile Gln Arg Ala Ser Gln Ser Asn Asn Phe Pro Asn Asp Ile
145                 150                 155                 160

Leu Asn Gly Ser Ala Ala Val Ile Ser Gln Ala Phe Ala Ala Gly Gln
                165                 170                 175

Phe Asp Ser Ile Arg Leu Thr Arg Leu Glu Ser Thr Met Val Asp Leu
            180                 185                 190

Ser Asn Cys Gln Gly Gly Met Glu Arg Ile Ala Asn Thr Pro Leu Pro
        195                 200                 205

Tyr Pro Tyr Val Tyr Phe Pro Arg Leu Phe Ser Thr Leu Phe Cys Ile
    210                 215                 220

Leu Met Pro Leu Ser Met Val Thr Thr Leu Gly Trp Phe Thr Pro Ala
225                 230                 235                 240

Ile Ser Thr Val Val Gly Cys Met Leu Leu Ala Met Asp Arg Ile Gly
                245                 250                 255

Thr Asp Leu Gln Ala Pro Phe Gly Asn Ser Gln His Arg Ile Arg Met
            260                 265                 270

Glu Asp Leu Cys Asn Thr Ile Glu Lys Asn Leu Gln Ser Met Phe Ser
        275                 280                 285

Ser Pro Glu Arg Gln Pro Leu Leu Ala Asp Leu Lys Ser Pro Val Pro
    290                 295                 300

Trp Arg Val Ala Asn Ala Ser Ile Gly Gly Leu Ser Arg Gln Lys Asn
305                 310                 315                 320

Arg Leu Gly Glu Gly Ala Arg Leu Ile Ala Ser Glu Ser Leu Leu Trp
                325                 330                 335

Ala Pro Phe Arg Ser Val Ala Asp Val Ala Pro Cys His Ala Ser Ala
            340                 345                 350

Tyr Leu Arg Arg Ala
        355
```

The DNA molecule of *ORF7* from the *Pseudomonas syringae* pv. tomato DC3000 CEL has a nucleotide sequence (SEQ. ID. No. 10) as follows:

```
atgtatatcc agcaatctgg cgcccaatca ggggttgccg ctaagacgca acacgataag 60
ccctcgtcat tgtccggact cgccccggt tcgtcggatg cgttcgcccg ttttcatccc 120
gaaaaggcgg gcgcctttgt cccattggag gggcatgaag aggtcttttt cgatgcgcgc 180
tcttcctttt cgtcggtcga tgccgctgat cttcccagtc ccgagcaggt acaaccccag 240
cttcattcgt tgcgtaccct gctaccggat ctgatggtct ctatcgcctc attacgtgac 300
ggcgccacgc aatacatcaa gaccagaatc aaggctatgg cggacaacag cataggcgcg 360
actgcgaaca tcgaagccaa aagaaagatt gcccaagagc acggctgtca gcttgtccac 420
ccgtttcacc agagcaaatt tctatttgaa aaaactatcg atgatagagc gtttgctgct 480
gactatggcc gcgcgggtgg cgacgggcac gcttgtctgg ggctatcagt aaattggtgt 540
cagagccgtg caaaagggca gtcggatgag gccttctttc acaaactgga ggactatcag 600
```

```
ggcgatgcat tgctacccag ggtaatgggc ttccagcata tcgagcagca ggcctattca 660
aacaagttgc agaacgcagc acctatgctt ctggacacac ttcccaagtt gggcatgaca 720
cttggaaaag ggctgggcag agcacagcac gcgcactatg cggttgctct ggaaaacctt 780
gatcgcgatc tcaaagcagt gttgcagccc ggtaaagacc agatgcttct gttttgagt 840
gatagccatg cgatggctct gcatcaggac agtcagggat gtctgcattt ttttgatcct 900
ctttttggcg tggttcaggc agacagcttc agcaacatga gccattttct tgctgatgtg 960
ttcaagcgcg acgtaggtac gcactggcgt ggcacggagc aacgtctgca actgagcgaa 1020
atggtgccca gagcagactt tcacttgcga taa                              1053
```

The protein or polypeptide encoded by *Pto* DC3000 CEL *ORF7* has an amino acid sequence (SEQ. ID. No. 11) as follows:

```
Met Tyr Ile Gln Gln Ser Gly Ala Gln Ser Gly Val Ala Ala Lys Thr
 1               5                  10                  15

Gln His Asp Lys Pro Ser Ser Leu Ser Gly Leu Ala Pro Gly Ser Ser
            20                  25                  30

Asp Ala Phe Ala Arg Phe His Pro Glu Lys Ala Gly Ala Phe Val Pro
        35                  40                  45

Leu Glu Gly His Glu Glu Val Phe Phe Asp Ala Arg Ser Ser Phe Ser
    50                  55                  60

Ser Val Asp Ala Ala Asp Leu Pro Ser Pro Glu Gln Val Gln Pro Gln
65                  70                  75                  80

Leu His Ser Leu Arg Thr Leu Leu Pro Asp Leu Met Val Ser Ile Ala
                85                  90                  95

Ser Leu Arg Asp Gly Ala Thr Gln Tyr Ile Lys Thr Arg Ile Lys Ala
            100                 105                 110

Met Ala Asp Asn Ser Ile Gly Ala Thr Ala Asn Ile Glu Ala Lys Arg
        115                 120                 125

Lys Ile Ala Gln Glu His Gly Cys Gln Leu Val His Pro Phe His Gln
    130                 135                 140

Ser Lys Phe Leu Phe Glu Lys Thr Ile Asp Asp Arg Ala Phe Ala Ala
145                 150                 155                 160

Asp Tyr Gly Arg Ala Gly Gly Asp Gly His Ala Cys Leu Gly Leu Ser
                165                 170                 175

Val Asn Trp Cys Gln Ser Arg Ala Lys Gly Gln Ser Asp Glu Ala Phe
            180                 185                 190

Phe His Lys Leu Glu Asp Tyr Gln Gly Asp Ala Leu Leu Pro Arg Val
        195                 200                 205

Met Gly Phe Gln His Ile Glu Gln Gln Ala Tyr Ser Asn Lys Leu Gln
    210                 215                 220

Asn Ala Ala Pro Met Leu Leu Asp Thr Leu Pro Lys Leu Gly Met Thr
225                 230                 235                 240

Leu Gly Lys Gly Leu Gly Arg Ala Gln His Ala His Tyr Ala Val Ala
                245                 250                 255

Leu Glu Asn Leu Asp Arg Asp Leu Lys Ala Val Leu Gln Pro Gly Lys
            260                 265                 270
```

```
Asp Gln Met Leu Leu Phe Leu Ser Asp Ser His Ala Met Ala Leu His
        275                 280                 285

Gln Asp Ser Gln Gly Cys Leu His Phe Phe Asp Pro Leu Phe Gly Val
    290                 295                 300

Val Gln Ala Asp Ser Phe Ser Asn Met Ser His Phe Leu Ala Asp Val
305                 310                 315                 320

Phe Lys Arg Asp Val Gly Thr His Trp Arg Gly Thr Glu Gln Arg Leu
                325                 330                 335

Gln Leu Ser Glu Met Val Pro Arg Ala Asp Phe His Leu Arg
            340                 345                 350
```

The DNA molecule of *ORF8* from the *Pseudomonas syringae* pv. tomato DC3000 CEL has a nucleotide sequence (SEQ. ID. No. 12) as follows:

```
atgcggcctg tcgaggcaaa agatcggctt tatcagtggc tgcgcaatcg aggcatcgat 60
gcgcaggagg gtcaacgcca caacgtaagg accgcgaatg gaagcgagtg tctgctctgg 120
ttgccagaac aggacacttc gttgttcatc ttcacacaga tcgaaaggct gacgatgccg 180
caggacaacg tcattttgat tctggcaatg gcgctgaatc tggagcctgc tcgcacaggt 240
ggcgctgcgc ttggctataa ccctgattca agggaactgt tgttgcgcag tgtgcactca 300
atggcggatc tggatgagac cggacttgat cacctcatga cgcgaattag cacattggcc 360
gtctcgttgc agcgctatct ggaagattat cgacgccagg agcaagccgg aaaaaccgcc 420
cagaaagagc ctcggttctt accggctgtc catctgaccc cacgaacgtt catgacctga 480
```

The protein or polypeptide encoded by *Pto* DC3000 CEL *ORF8* has an amino acid sequence (SEQ. ID. No. 13) as follows:

```
Met Arg Pro Val Glu Ala Lys Asp Arg Leu Tyr Gln Trp Leu Arg Asn
  1               5                  10                  15

Arg Gly Ile Asp Ala Gln Glu Gly Gln Arg His Asn Val Arg Thr Ala
            20                  25                  30

Asn Gly Ser Glu Cys Leu Leu Trp Leu Pro Glu Gln Asp Thr Ser Leu
        35                  40                  45

Phe Ile Phe Thr Gln Ile Glu Arg Leu Thr Met Pro Gln Asp Asn Val
    50                  55                  60

Ile Leu Ile Leu Ala Met Ala Leu Asn Leu Glu Pro Ala Arg Thr Gly
65                  70                  75                  80

Gly Ala Ala Leu Gly Tyr Asn Pro Asp Ser Arg Glu Leu Leu Leu Arg
                85                  90                  95

Ser Val His Ser Met Ala Asp Leu Asp Glu Thr Gly Leu Asp His Leu
            100                 105                 110

Met Thr Arg Ile Ser Thr Leu Ala Val Ser Leu Gln Arg Tyr Leu Glu
        115                 120                 125

Asp Tyr Arg Arg Gln Glu Gln Ala Gly Lys Thr Ala Gln Lys Glu Pro
    130                 135                 140
```

```
Arg Phe Leu Pro Ala Val His Leu Thr Pro Arg Thr Phe Met Thr
145                 150                 155
```

The DNA molecule of *ORF9* from the *Pseudomonas syringae* pv. tomato DC3000 CEL has a nucleotide sequence (SEQ. ID. No. 14) as follows:

```
atgcttaaaa aatgcctgct actggttata tcaatgtcac ttggcggctg ctggagcctg 60
atgattcatc tggacggcga gcgttgcatc tatcccggca ctcgccaagg ttgggcgtgg 120
ggaacccata acggagggca gagttggccc atacttatag acgtgccgtt ttccctcgcg 180
ttggacacac tgctgctgcc ctacgacctc accgcttttc tgcccgaaaa tcttggcggt 240
gatgaccgca aatgtcagtt cagtggagga ttgaacgtgc tcggttga              288
```

The protein or polypeptide encoded by *Pto* DC3000 CEL *ORF9* has an amino acid sequence (SEQ. ID. No. 15) as follows:

```
Met Leu Lys Lys Cys Leu Leu Leu Val Ile Ser Met Ser Leu Gly Gly
  1               5                  10                  15

Cys Trp Ser Leu Met Ile His Leu Asp Gly Glu Arg Cys Ile Tyr Pro
            20                  25                  30

Gly Thr Arg Gln Gly Trp Ala Trp Gly Thr His Asn Gly Gly Gln Ser
        35                  40                  45

Trp Pro Ile Leu Ile Asp Val Pro Phe Ser Leu Ala Leu Asp Thr Leu
    50                  55                  60

Leu Leu Pro Tyr Asp Leu Thr Ala Phe Leu Pro Glu Asn Leu Gly Gly
65                  70                  75                  80

Asp Asp Arg Lys Cys Gln Phe Ser Gly Gly Leu Asn Val Leu Gly
                85                  90                  95
```

The DNA molecule of *ORF10* from the *Pseudomonas syringae* pv. tomato DC3000 CEL has a nucleotide sequence (SEQ. ID. No. 16) as follows:

```
atgaaacagg tagaagtcca gatcattact gaattgcctt gtcaggttct gatcctggag 60
caagaggcag tagcagaggg cttcaggttt cttacccgct tgatcgagga gtggaggtcc 120
ggaaagaatc gattcgaggc caagggtgaa tgcctcatgg tcgtacttct ggacggcgct 180
ctggcaggta tcggaggcct ttcgcgtgat ccgcatgccc ggggtgatat gggcaggcta 240
cgacggttat acgtcgcaag cgcatcaaga ggtcaaggcc ttggaaagac tctggtgaat 300
cgacttgtgg agcatgcggc gcaggaattt ttcgccgtgc gcctgttcac tgatactccg 360
agcggagcaa aattttactt acgttgcggc tttcaggcag ttgacgaggt gcatgccacg 420
catataaagc ttttaaggcg ggtttga                                     447
```

The protein or polypeptide encoded by *Pto* DC3000 CEL *ORF10* has an amino acid sequence (SEQ. ID. No. 17) as follows:

```
Met Lys Gln Val Glu Val Gln Ile Ile Thr Glu Leu Pro Cys Gln Val
  1               5                  10                  15
```

```
Leu Ile Leu Glu Gln Glu Ala Val Ala Glu Gly Phe Arg Phe Leu Thr
            20                  25                  30

Arg Leu Ile Glu Glu Trp Arg Ser Gly Lys Asn Arg Phe Glu Ala Lys
        35                  40                  45

Gly Glu Cys Leu Met Val Val Leu Leu Asp Gly Ala Leu Ala Gly Ile
    50                  55                  60

Gly Gly Leu Ser Arg Asp Pro His Ala Arg Gly Asp Met Gly Arg Leu
65                  70                  75                  80

Arg Arg Leu Tyr Val Ala Ser Ala Ser Arg Gly Gln Gly Leu Gly Lys
                85                  90                  95

Thr Leu Val Asn Arg Leu Val Glu His Ala Ala Gln Glu Phe Phe Ala
            100                 105                 110

Val Arg Leu Phe Thr Asp Thr Pro Ser Gly Ala Lys Phe Tyr Leu Arg
        115                 120                 125

Cys Gly Phe Gln Ala Val Asp Glu Val His Ala Thr His Ile Lys Leu
    130                 135                 140

Leu Arg Arg Val
145
```

A DNA molecule which contains the EEL of *Pseudomonas syringae* pv. tomato DC3000 has a nucleotide sequence (SEQ. ID. No. 18) as follows:

```
ggatccagcg gcgtattgtc gtggcgatgg aacgcgttac ggattttcag cacaccggta 60
tcgatgaaca ggtggccgtt gcgggcgttg cgggtcggca tgacacaatc gaacatatca 120
acgccacggc gcacaccttc gaccagatct tcgggcttgc ctacacccat caagtaacga 180
ggtttgtctg ctggcataag gcccggcagg taatccagca ccttgatcat ctcgtgcttg 240
ggctcgccca ccgacagacc gccaatcgcc aggccgtcaa agccgatctc atccaggcct 300
tcgagcgaac gcttgcgcag gttctcgtgc atgccaccct gaacaatgcc gaacagcgcg 360
gcagtgtttt cgccgtgcgc gaccttggag cgcttggccc agcgcaacga cagctccatg 420
gagacacgtg ctacgtcttc gtcggccggg tacggcgtgc actcatcgaa aatcatcacg 480
acgtccgaac ccaggtcacg ctggacctgc atcgactctt ccgggcccat gaacaccttg 540
gcaccatcga ccggagaggc gaaggtcacg ccctcctcct tgatcttgcg catggcgccc 600
aggctgaaca cctgaaaacc gccagagtcg gtcagaatcg gccctttcca ctgcatgaaa 660
tcgtgcaggt cgccgtggcc cttgatgacc tcggtgcccg gacgcagcca caagtggaag 720
gtgttgccca gaatcatctg cgcaccggtg gcctcgatat cacgcggcaa catgcccttg 780
accgtgccgt aggtgcccac cggcatgaac gccggggtct cgaccacgcc acgcggaaag 840
gtcaggcgac cgcgacgggc cttgccgtcg gtggccaaca actcgaaaga catacgacag 900
gtgcgactca tgcgtgatcc tctggtgccg attcctgtgg ggccgtcggc gcgggattgc 960
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```

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```

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acccttttcaa tgttgatttg ncaaataagg gattnnccca aaaggtttng ctttnggg   11458
```

Several undefined nucleotides exist in SEQ. ID. No. 18, however these appear to be present in intergenic regions. The EEL of *Pseudomonas syringae* pv. tomato DC3000 contains a number of ORFs. One of the products encoded by the EEL is a homolog of TnpA' from *P. stutzeri*. An additional four products are produced by *ORF1-4*, respectively. The nucleotide sequences for a number of these ORFs and their encoded protein or polypeptide products are provided below.

The DNA molecule of *ORF1* from the *Pseudomonas syringae* pv. tomato DC3000 EEL has a nucleotide sequence (SEQ. ID. No. 19) as follows:

```
atgagacccg tcggtggacc ggctccaggc tattatccgc caacctatga agctgagcgt 60
cccactgcgc aagctgcagg aaacgatcgc gcccgatctt cacaggccag ttcctctcca 120
gcagccagcg ttgcgccaga gactccaatg ctgggggacc tgaagcgctt tccagccggg 180
cgctatccgg atatgaaggt agaaaatatc cggctgaaaa tcgaggggca ggagcctggc 240
ggaaaggatg gcgtaaagca caccagaagg cgtaagccgg acgcagcagg cagcagtcat 300
gtgcacggcg gccagagcgt ggcctcgacc tcggcttcag ctcaaagcaa agcattgcag 360
gatacgaact tcaaggcgag cgatcttgcc gagctcgcgc gctggtgtga gagcccgcac 420
ccctatgcgc tggcaccctc aaaagcagcg gggaaaagca gccaactgtc tgcaaatgtt 480
gtgagcatcc tgttgcaaga aggcaagcac gcccttgaac agcgccttga ggctcaaggt 540
ctcaagctgg ccgacgttgt tgtctcggaa ggtcgggacc accttcatat aaatctcaat 600
taccttgaaa tggacagttg tctggggacg tccaagggtt tatgggcacc tgacagtaat 660
gacaagaaac tgattgccaa ggcagcgcgt tattttgatg atttcaacgc gcaaaagtta 720
cctgagctgg cgccgttgac gaagatgaaa agcaaggaca gtctcggtgt catgcgcgag 780
ctgttacgtg atgcgccggg gcttgttatt ggtgagggtc acaattcaac gtccagcaag 840
cgtgaactga tcaataacat gaagagcttg aaggccagtg gcgtgaccac gctttttatg 900
gagcacctct gcgccgagtc acatgacaag gcgctcaata attacctgag cgcgcccaaa 960
ggcagtccga tgcctgccag gctgaaaaac tacctcgatt tgcagagtca gggtcatcag 1020
```

```
gccccggaag agctccacac gaaatataac ttcaccacct tggtggaagc ggccaagcac 1080
gccgggttgc gcgttgtctc gctggataca acgtccacct atatggcccc ggagaaagct 1140
gagataaagc gtgcccaagc catgaattac tacgcagcag aaaaaataag gctgagcaaa 1200
ccggaaggta agtgggtcgc ttttgtcggg gcaacgcacg ccacttcctg tgacggagtc 1260
ccagggttgg cagagttgca tggggtacgc agtctggtga tcgatgatct gggcctcaag 1320
tcccgagcga ccgtcgatat caatgtgaaa aactacggcg gcaagctgaa tccagacgtg 1380
aggctttcct ataaggtctg a                                          1401
```

The protein or polypeptide encoded by *Pto* DC3000 EEL ORF1 has an amino acid sequence (SEQ. ID. No. 20) as follows:

```
Met Arg Pro Val Gly Gly Pro Ala Pro Gly Tyr Tyr Pro Pro Thr Tyr
  1               5                  10                  15

Glu Ala Glu Arg Pro Thr Ala Gln Ala Ala Gly Asn Asp Arg Ala Arg
            20                  25                  30

Ser Ser Gln Ala Ser Ser Ser Pro Ala Ala Ser Val Ala Pro Glu Thr
        35                  40                  45

Pro Met Leu Gly Asp Leu Lys Arg Phe Pro Ala Gly Arg Tyr Pro Asp
    50                  55                  60

Met Lys Val Glu Asn Ile Arg Leu Lys Ile Glu Gly Gln Glu Pro Gly
65                  70                  75                  80

Gly Lys Asp Gly Val Lys His Thr Arg Arg Arg Lys Pro Asp Ala Ala
                85                  90                  95

Gly Ser Ser His Val His Gly Gly Gln Ser Val Ala Ser Thr Ser Ala
            100                 105                 110

Ser Ala Gln Ser Lys Ala Leu Gln Asp Thr Asn Phe Lys Ala Ser Asp
        115                 120                 125

Leu Ala Glu Leu Ala Arg Trp Cys Glu Ser Pro His Pro Tyr Ala Leu
    130                 135                 140

Ala Pro Ser Lys Ala Ala Gly Lys Ser Ser Gln Leu Ser Ala Asn Val
145                 150                 155                 160

Val Ser Ile Leu Leu Gln Glu Gly Lys His Ala Leu Glu Gln Arg Leu
                165                 170                 175

Glu Ala Gln Gly Leu Lys Leu Ala Asp Val Val Val Ser Glu Gly Arg
            180                 185                 190

Asp His Leu His Ile Asn Leu Asn Tyr Leu Glu Met Asp Ser Cys Leu
        195                 200                 205

Gly Thr Ser Lys Gly Leu Trp Ala Pro Asp Ser Asn Asp Lys Lys Leu
    210                 215                 220

Ile Ala Lys Ala Ala Arg Tyr Phe Asp Asp Phe Asn Ala Gln Lys Leu
225                 230                 235                 240

Pro Glu Leu Ala Pro Leu Thr Lys Met Lys Ser Lys Asp Ser Leu Gly
                245                 250                 255

Val Met Arg Glu Leu Leu Arg Asp Ala Pro Gly Leu Val Ile Gly Glu
            260                 265                 270
```

```
Gly His Asn Ser Thr Ser Ser Lys Arg Glu Leu Ile Asn Asn Met Lys
        275                 280                 285

Ser Leu Lys Ala Ser Gly Val Thr Thr Leu Phe Met Glu His Leu Cys
    290                 295                 300

Ala Glu Ser His Asp Lys Ala Leu Asn Asn Tyr Leu Ser Ala Pro Lys
305                 310                 315                 320

Gly Ser Pro Met Pro Ala Arg Leu Lys Asn Tyr Leu Asp Leu Gln Ser
                325                 330                 335

Gln Gly His Gln Ala Pro Glu Glu Leu His Thr Lys Tyr Asn Phe Thr
            340                 345                 350

Thr Leu Val Glu Ala Ala Lys His Ala Gly Leu Arg Val Val Ser Leu
        355                 360                 365

Asp Thr Thr Ser Thr Tyr Met Ala Pro Glu Lys Ala Glu Ile Lys Arg
    370                 375                 380

Ala Gln Ala Met Asn Tyr Tyr Ala Ala Glu Lys Ile Arg Leu Ser Lys
385                 390                 395                 400

Pro Glu Gly Lys Trp Val Ala Phe Val Gly Ala Thr His Ala Thr Ser
                405                 410                 415

Cys Asp Gly Val Pro Gly Leu Ala Glu Leu His Gly Val Arg Ser Leu
            420                 425                 430

Val Ile Asp Asp Leu Gly Leu Lys Ser Arg Ala Thr Val Asp Ile Asn
        435                 440                 445

Val Lys Asn Tyr Gly Gly Lys Leu Asn Pro Asp Val Arg Leu Ser Tyr
    450                 455                 460

Lys Val
465
```

The DNA molecule of *ORF2* from the *Pseudomonas syringae* pv. tomato DC3000 EEL has a nucleotide sequence (SEQ. ID. No. 21) as follows:

```
atgcaaaaga cgaccctatg ggctttagcc tttgcaatgt tggcagggtg tggggtttcg 60
gggccggcgc cgggaagtga tattcagggt gcccaggcag agatgaaaac acccgttaaa 120
ctaaatctgg atgcctacac ctcaaaaaaa ctggatgctg tgctggaagc ccgcaccaac 180
aaaagttata tgaataaagg tcagctgatc gaccttgtat caggagcgtt tttaggaaca 240
ccgtaccgct caaacatgtt ggtgggctca gcgaatgtac ctgaacaatt agtcatcgac 300
ttcagaggtc tggattgttt tgcttatctg gattacgtcg aagcgtttcg aagatcaaca 360
tcgcagcagg attttgtgag gaatctcgtt caggttcgtt acaagggtgg cgatgttgac 420
tttttgaatc gcaagcactt tttcacggat tgggcttacg gaacggcata ccctgtggcg 480
gatgacatta ccgcgcagat aagccccggt gcggtaagtg tcagaaaacg ccttaatgaa 540
agggccaaag gcaaagtcta tctgccaggg ttgcctgtgg ttgagcgtag catgacgtat 600
atcccgagcc gccttgtcga cagtcaggtg gtgagccacc tgcgcaccgg tgattacatt 660
ggcatttaca cccccgcttc ccgggctgga tgtgacacac gtcggtttct ttatcgtgac 720
ggataa                                                          726
```

The protein or polypeptide encoded by *Pto* DC3000 EEL ORF2 has an amino acid sequence (SEQ. ID. No. 22) as follows:

```
Met Gln Lys Thr Thr Leu Trp Ala Leu Ala Phe Ala Met Leu Ala Gly
  1               5                  10                  15

Cys Gly Val Ser Gly Pro Ala Pro Gly Ser Asp Ile Gln Gly Ala Gln
             20                  25                  30

Ala Glu Met Lys Thr Pro Val Lys Leu Asn Leu Asp Ala Tyr Thr Ser
         35                  40                  45

Lys Lys Leu Asp Ala Val Leu Glu Ala Arg Thr Asn Lys Ser Tyr Met
     50                  55                  60

Asn Lys Gly Gln Leu Ile Asp Leu Val Ser Gly Ala Phe Leu Gly Thr
 65                  70                  75                  80

Pro Tyr Arg Ser Asn Met Leu Val Gly Ser Ala Asn Val Pro Glu Gln
                 85                  90                  95

Leu Val Ile Asp Phe Arg Gly Leu Asp Cys Phe Ala Tyr Leu Asp Tyr
            100                 105                 110

Val Glu Ala Phe Arg Arg Ser Thr Ser Gln Gln Asp Phe Val Arg Asn
        115                 120                 125

Leu Val Gln Val Arg Tyr Lys Gly Gly Asp Val Asp Phe Leu Asn Arg
    130                 135                 140

Lys His Phe Phe Thr Asp Trp Ala Tyr Gly Thr Ala Tyr Pro Val Ala
145                 150                 155                 160

Asp Asp Ile Thr Ala Gln Ile Ser Pro Gly Ala Val Ser Val Arg Lys
                165                 170                 175

Arg Leu Asn Glu Arg Ala Lys Gly Lys Val Tyr Leu Pro Gly Leu Pro
            180                 185                 190

Val Val Glu Arg Ser Met Thr Tyr Ile Pro Ser Arg Leu Val Asp Ser
        195                 200                 205

Gln Val Val Ser His Leu Arg Thr Gly Asp Tyr Ile Gly Ile Tyr Thr
    210                 215                 220

Pro Ala Ser Arg Ala Gly Cys Asp Thr Arg Arg Phe Leu Tyr Arg Asp
225                 230                 235                 240

Gly
```

The DNA molecule of *ORF3* from the *Pseudomonas syringae* pv. tomato DC3000 EEL has a nucleotide sequence (SEQ. ID. No. 23) as follows:

```
atgcgcgcgt ataaaaacct gacggcaaag atcggcggct ttctgcttgc gctgacgatc 60
attggcactt cgctacctgc atttgccgta aacgattgtg atctggacaa cgacaacagc 120
accggtgcca cgtgtggcgg caacgacaag gatctggata acgacaacgt gactgacgcg 180
gcatttggcg gcaacgacaa ggatatggac aatgaccacc acaccgacgc ggcatttggg 240
ggtaacgaca aggacctgga caacgatcac catacggatg cagcgtttgg cggtaacgac 300
aaagatctcg acaacgacaa caaaaccgat gcggctttcg gtggaaatga ccgcgatctt 360
gataacgaca acaacaccga caactacaac ggcacgccgt ctgccgctaa aaagtag    417
```

The protein or polypeptide encoded by *Pto* DC3000 EEL *ORF3* has an amino acid sequence (SEQ. ID. No. 24) as follows:

```
Met Arg Ala Tyr Lys Asn Leu Thr Ala Lys Ile Gly Gly Phe Leu Leu
 1               5                  10                  15

Ala Leu Thr Ile Ile Gly Thr Ser Leu Pro Ala Phe Ala Val Asn Asp
            20                  25                  30

Cys Asp Leu Asp Asn Asp Asn Ser Thr Gly Ala Thr Cys Gly Gly Asn
        35                  40                  45

Asp Lys Asp Leu Asp Asn Asp Asn Val Thr Asp Ala Ala Phe Gly Gly
    50                  55                  60

Asn Asp Lys Asp Met Asp Asn Asp His His Thr Asp Ala Ala Phe Gly
65                  70                  75                  80

Gly Asn Asp Lys Asp Leu Asp Asn Asp His His Thr Asp Ala Ala Phe
                85                  90                  95

Gly Gly Asn Asp Lys Asp Leu Asp Asn Asp Asn Lys Thr Asp Ala Ala
            100                 105                 110

Phe Gly Gly Asn Asp Arg Asp Leu Asp Asn Asp Asn Asn Thr Asp Asn
        115                 120                 125

Tyr Asn Gly Thr Pro Ser Ala Ala Lys Lys
    130                 135
```

P. s. syringae pv. *tomato* DC3000 EEL ORF3 has now been shown to significantly reduce virulence when mutated. Perhaps more interestingly, overexpression strongly increases lesion size. Hence, this effector is biologically active and appears to have a key role in symptom production.

The DNA molecule of *ORF4* from the *Pseudomonas syringae* pv. tomato DC3000 EEL has a nucleotide sequence (SEQ. ID. No. 25) as follows:

```
atgaacaaga tcgtctacgt aaaagcttac ttcaaaccca ttggggagga agtctcggtt 60
aaagtaccta caggcgaaat taaaaagggc tttttcggcg acaaggaaat catgaaaaaa 120
gagacccagt ggcagcaaac cgggtggtct gattgtcaga tagacggtga acggctatcg 180
aaagacgtcg aagacgcagt ggcgcaactc aatgctgacg gttatgagat tcaaacggta 240
ttgcctatat tgtccggggc ttatgattat gcgctcaaat accgatacga aatacgtcac 300
aatagaactg aactaagccc aggagaccag tcctatgtct tcggctatgg ctacagcttc 360
accgaaggcg tgacgctggt ggcgaaaaaa tttcagtcgt ctgcaagctg a          411
```

The protein or polypeptide encoded by *Pto* DC3000 EEL *ORF4* has an amino acid sequence (SEQ. ID. No. 26) as follows:

```
Met Asn Lys Ile Val Tyr Val Lys Ala Tyr Phe Lys Pro Ile Gly Glu
 1               5                  10                  15

Glu Val Ser Val Lys Val Pro Thr Gly Glu Ile Lys Lys Gly Phe Phe
            20                  25                  30

Gly Asp Lys Glu Ile Met Lys Lys Glu Thr Gln Trp Gln Gln Thr Gly
        35                  40                  45
```

```
Trp Ser Asp Cys Gln Ile Asp Gly Glu Arg Leu Ser Lys Asp Val Glu
     50                  55                  60

Asp Ala Val Ala Gln Leu Asn Ala Asp Gly Tyr Glu Ile Gln Thr Val
 65                  70                  75                  80

Leu Pro Ile Leu Ser Gly Ala Tyr Asp Tyr Ala Leu Lys Tyr Arg Tyr
                 85                  90                  95

Glu Ile Arg His Asn Arg Thr Glu Leu Ser Pro Gly Asp Gln Ser Tyr
            100                 105                 110

Val Phe Gly Tyr Gly Tyr Ser Phe Thr Glu Gly Val Thr Leu Val Ala
        115                 120                 125

Lys Lys Phe Gln Ser Ser Ala Ser
    130                 135
```

The EEL of *Pseudomonas syringae* pv. syringae B728a contains a number of ORFs. Two of the open reading frames appear to be mobile genetic elements without comparable homologs in EELs of other *Pseudomonas syringae* variants. An additional four products are produced by *ORF1-2* and *ORF5-6*, respectively. The nucleotide sequences for a number of these ORFs and their encoded protein or polypeptide products are provided below.

The DNA molecule of *ORF1* from the *Pseudomonas syringae* pv. syringae B728a EEL has a nucleotide sequence (SEQ. ID. No. 27) as follows:

```
atgggttgcg tatcgtcaaa agcatctgtc atttcttcgg acagctttcg cgcatcatat 60
acaaactctc cagaggcatc ctcagtccat caacgagcca ggacgccaag gtgcggtgag 120
cttcaggggc cccaagtgag cagattgatg ccttaccagc aggcgttagt aggtgtggcc 180
cgatggccta atccgcattt taacagggac gatgcgcccc accagatgga gtatggagaa 240
tcgttctacc ataaaagccg agagcttggt gcgtcggtcg ccaatggaga gatagaaacg 300
tttcaggagc tctggagtga agctcgtgat tggagagctt ccagagcagg ccaagatgct 360
cggcttttta gttcatcgcg tgatcccaac tcttcacggg cgtttgttac gcctataact 420
ggaccatacg aatttttaaa agatagattc gcaaaccgta aagatggaga aaagcataag 480
atgatggatt ttctcccaca cagcaatacg tttaggtttc atgggaaaat tgacggtgag 540
cgacttcctc tcacctggat ctcgataagt tctgatcgtc gtgccgacag aacaaaggat 600
ccttaccaaa ggttgcgcga ccaaggcatg aacgatgtgg gtgagcctaa tgtgatgttg 660
cacacccaag ccgagtatgt gcccaaaatt atgcaacatg tggagcatct ttataaggcc 720
gctacggatg ctgcattgtc cgatgccaat gcgctgaaaa aactcgcaga gatacattgg 780
tggacggtac aagctgttcc cgactttcgt ggaagtgcag ctaaggctga gctctgcgtg 840
cgctccattg cccaggcaag gggcatggac ctgccgccga tgagactcgg catcgtgccg 900
gatctggaag cgcttacgat gcctttgaaa gactttgtga aaagttacga agggttcttc 960
gaacataact ga                                                    972
```

The protein or polypeptide encoded by *Psy* B728a EEL *ORF1* has an amino acid sequence (SEQ. ID. No. 28) as follows:

```
Met Gly Cys Val Ser Ser Lys Ala Ser Val Ile Ser Ser Asp Ser Phe
  1               5                  10                  15

Arg Ala Ser Tyr Thr Asn Ser Pro Glu Ala Ser Ser Val His Gln Arg
            20                  25                  30
```

```
Ala Arg Thr Pro Arg Cys Gly Glu Leu Gln Gly Pro Gln Val Ser Arg
          35                  40                  45

Leu Met Pro Tyr Gln Gln Ala Leu Val Gly Val Ala Arg Trp Pro Asn
      50                  55                  60

Pro His Phe Asn Arg Asp Asp Ala Pro His Gln Met Glu Tyr Gly Glu
 65                  70                  75                  80

Ser Phe Tyr His Lys Ser Arg Glu Leu Gly Ala Ser Val Ala Asn Gly
                 85                  90                  95

Glu Ile Glu Thr Phe Gln Glu Leu Trp Ser Glu Ala Arg Asp Trp Arg
            100                 105                 110

Ala Ser Arg Ala Gly Gln Asp Ala Arg Leu Phe Ser Ser Ser Arg Asp
        115                 120                 125

Pro Asn Ser Ser Arg Ala Phe Val Thr Pro Ile Thr Gly Pro Tyr Glu
    130                 135                 140

Phe Leu Lys Asp Arg Phe Ala Asn Arg Lys Asp Gly Glu Lys His Lys
145                 150                 155                 160

Met Met Asp Phe Leu Pro His Ser Asn Thr Phe Arg Phe His Gly Lys
                165                 170                 175

Ile Asp Gly Glu Arg Leu Pro Leu Thr Trp Ile Ser Ile Ser Ser Asp
            180                 185                 190

Arg Arg Ala Asp Arg Thr Lys Asp Pro Tyr Gln Arg Leu Arg Asp Gln
        195                 200                 205

Gly Met Asn Asp Val Gly Glu Pro Asn Val Met Leu His Thr Gln Ala
    210                 215                 220

Glu Tyr Val Pro Lys Ile Met Gln His Val Glu His Leu Tyr Lys Ala
225                 230                 235                 240

Ala Thr Asp Ala Ala Leu Ser Asp Ala Asn Ala Leu Lys Lys Leu Ala
                245                 250                 255

Glu Ile His Trp Trp Thr Val Gln Ala Val Pro Asp Phe Arg Gly Ser
            260                 265                 270

Ala Ala Lys Ala Glu Leu Cys Val Arg Ser Ile Ala Gln Ala Arg Gly
        275                 280                 285

Met Asp Leu Pro Pro Met Arg Leu Gly Ile Val Pro Asp Leu Glu Ala
    290                 295                 300

Leu Thr Met Pro Leu Lys Asp Phe Val Lys Ser Tyr Glu Gly Phe Phe
305                 310                 315                 320

Glu His Asn
```

As indicated in Table 1 (see Example 2), the DNA molecule encoding this protein or polypeptide bears significant homology to the nucleotide sequence from *Pseudomonas syringae* pv. *phaseolicola* which encodes AvrPphC.

The DNA molecule of *ORF2* from the *Pseudomonas syringae* pv. syringae B728a EEL has a nucleotide sequence (SEQ. ID. No. 29) as follows:

```
atgagaattc acagttccgg tcatggcatc tccggaccag tatcctctgc agaaaccgtt 60
gaaaaggccg tgcaatcatc ggcccaagcg cagaatgaag cgtctcacag cggtccatca 120
gaacatcctg aatcccgctc ctgtcaggca cgcccgaact acccttattc gtcagtcaaa 180
acacggttac cccctgttgc gtctgcaggg cagtcgctgt ctgagacacc ctcttcattg 240
cctggctacc tgctgttacg tcggcttgat cgtcgtccgc tggaccagga cgcaataaag 300
gggcttattc ctgctgatga agcagtgggc gaagcgcgcc gcgcgttgcc cttcggcagg 360
ggcaacattg atgtggatgc gcaacgctcc aacctggaaa gcggggcccg cacgctcgcc 420
gcaagacgcc tgagaaaaga cgccgagacg gcgggtcatg agccgatgcc cgagaacgaa 480
gacatgaact ggcatgtgct ggttgccatg tcgggtcagg tgttcggggc tggcaactgt 540
ggcgaacatg cccgtatagc gagctttgcc tacggtgcat cggctcagga aaaaggacgc 600
gctggcgatg aaaatattca tctggctgcg cagagcgggg aagatcatgt ctgggctgaa 660
acggatgatt ccagcgctgg ctcttcgcct attgtcatgg acccctggtc aaacggtcct 720
gccgtttttg cagaggacag tcggtttgct aaagataggc gcgcggtaga gcgaacggat 780
tcgttcacgc tttcaaccgc tgccaaagca ggcaagatta cacgagagac agccgagaag 840
gcgctgaccc aagcgaccag ccgtttgcag caacgtcttg ctgatcagca ggcgcaagtc 900
tcgccggttg aaggtggtcg ctatcggcaa gaaaactcgg tgcttgatga tgcgttcgcc 960
cgacgagtca gtgacatgtt gaacaatgcc gatccacggc gtgcattgca ggtggaaatc 1020
gaggcgtccg gagttgcaat gtcgctgggt gcccaaggcg tcaagacggt cgtccgacag 1080
gcgccaaaag tggtcaggca agccagaggc gtcgcatctg ctaaaggtat gtctccgcga 1140
gcaacctga                                                        1149
```

The protein or polypeptide encoded by *Psy* B728a EEL *ORF2* has an amino acid sequence (SEQ. ID. No. 30) as follows:

```
Met Arg Ile His Ser Ser Gly His Gly Ile Ser Gly Pro Val Ser Ser
  1               5                  10                  15

Ala Glu Thr Val Glu Lys Ala Val Gln Ser Ser Ala Gln Ala Gln Asn
             20                  25                  30

Glu Ala Ser His Ser Gly Pro Ser Glu His Pro Glu Ser Arg Ser Cys
         35                  40                  45

Gln Ala Arg Pro Asn Tyr Pro Tyr Ser Ser Val Lys Thr Arg Leu Pro
     50                  55                  60

Pro Val Ala Ser Ala Gly Gln Ser Leu Ser Glu Thr Pro Ser Ser Leu
 65                  70                  75                  80

Pro Gly Tyr Leu Leu Leu Arg Arg Leu Asp Arg Arg Pro Leu Asp Gln
                 85                  90                  95

Asp Ala Ile Lys Gly Leu Ile Pro Ala Asp Glu Ala Val Gly Glu Ala
            100                 105                 110

Arg Arg Ala Leu Pro Phe Gly Arg Gly Asn Ile Asp Val Asp Ala Gln
        115                 120                 125

Arg Ser Asn Leu Glu Ser Gly Ala Arg Thr Leu Ala Ala Arg Arg Leu
    130                 135                 140

Arg Lys Asp Ala Glu Thr Ala Gly His Glu Pro Met Pro Glu Asn Glu
145                 150                 155                 160

Asp Met Asn Trp His Val Leu Val Ala Met Ser Gly Gln Val Phe Gly
                165                 170                 175
```

```
Ala Gly Asn Cys Gly Glu His Ala Arg Ile Ala Ser Phe Ala Tyr Gly
           180                 185                 190

Ala Ser Ala Gln Glu Lys Gly Arg Ala Gly Asp Glu Asn Ile His Leu
       195                 200                 205

Ala Ala Gln Ser Gly Glu Asp His Val Trp Ala Glu Thr Asp Asp Ser
   210                 215                 220

Ser Ala Gly Ser Ser Pro Ile Val Met Asp Pro Trp Ser Asn Gly Pro
225                 230                 235                 240

Ala Val Phe Ala Glu Asp Ser Arg Phe Ala Lys Asp Arg Arg Ala Val
                245                 250                 255

Glu Arg Thr Asp Ser Phe Thr Leu Ser Thr Ala Ala Lys Ala Gly Lys
           260                 265                 270

Ile Thr Arg Glu Thr Ala Glu Lys Ala Leu Thr Gln Ala Thr Ser Arg
       275                 280                 285

Leu Gln Gln Arg Leu Ala Asp Gln Gln Ala Gln Val Ser Pro Val Glu
   290                 295                 300

Gly Gly Arg Tyr Arg Gln Glu Asn Ser Val Leu Asp Asp Ala Phe Ala
305                 310                 315                 320

Arg Arg Val Ser Asp Met Leu Asn Asn Ala Asp Pro Arg Arg Ala Leu
                325                 330                 335

Gln Val Glu Ile Glu Ala Ser Gly Val Ala Met Ser Leu Gly Ala Gln
           340                 345                 350

Gly Val Lys Thr Val Val Arg Gln Ala Pro Lys Val Val Arg Gln Ala
       355                 360                 365

Arg Gly Val Ala Ser Ala Lys Gly Met Ser Pro Arg Ala Thr
   370                 375                 380
```

As indicated in Table 1 (see Example 2), the DNA molecule encoding this protein or polypeptide bears significant homology to the nucleotide sequence from *Pseudomonas syringae* pv. *phaseolicola* which encodes AvrPphE.

The DNA molecule of *ORF5* from the *Pseudomonas syringae* pv. syringae B728a EEL has a nucleotide sequence (SEQ. ID. No. 31) as follows:

```
atgaatatct caggtccgaa cagacgtcag gggactcagg cagagaacac tgaaagcgct 60
tcgtcatcat cggtaactaa cccaccgcta cagcgtggcg agggcagacg tctgcgacgt 120
caggatgcgc tgccaacgga tatcagatac aacgccaacc agacagcgac atcaccgcaa 180
aacgcgcgcg cggcaggaag atatgaatca ggggccagct catccggcgc gaatgatact 240
ccgcaggctg aaggttcaat gccttcgtcg tccgcccttt tacaatttcg cctcgccggc 300
gggcggaacc attctgagct ggaaaatttt catactatga tgctgaactc accgaaagca 360
tcacggggag atgctatacc tgagaagccc gaagcaatac ctaagcgcct actggagaag 420
atggaaccga ttaacctggc ccagttagct ttgcgtgata aggatctgca tgaatatgcc 480
gtaatggtct gtaaccaagt gaaaaagggt gaaggtccga actccaatat tacgcaagga 540
gatatcaagt tactgccgct gttcgccaaa gcggaaaata caagaaatcc cggcttgaat 600
ctgcatacat tcaaaagtca taaagactgt taccaggcga taaaagagca aaacagggat 660
attcaaaaaa acaagcaatc gctgagtatg cgggttgttt acccccccatt caaaaagatg 720
ccagaccacc atatagcctt ggatatccaa ctgagatacg gccatcgacc gtcgattgtc 780
ggctttgagt ctgcccctgg gaacattata gatgctgcag aaagggaaat actttcagca 840
```

```
ttaggcaacg tcaaaatcaa aatggtagga aattttcttc aatactcgaa aactgactgc 900
accatgtttg cgcttaataa cgccctgaaa gcttttaaac atcacgaaga atataccgcc 960
cgtctgcaca atggagaaaa gcaggtgcct atcccggcga ccttcttgaa acatgctcag 1020
tcaaaaagct tagtggagaa tcacccggaa aaagatacca ccgtcactaa agaccagggc 1080
ggtctgcata tggaaacgct attacacaga aaccgtgcct accgggcgca acgatctgcc 1140
ggtcagcacg ttacctctat tgaaggtttc agaatgcagg aaataaagag agcaggtgac 1200
ttccttgccg caaacagggt ccgggccaag ccttga                          1236
```

The protein or polypeptide encoded by *Psy* B728a EEL *ORF5* has an amino acid sequence (SEQ. ID. No. 32) as follows:

```
Met Asn Ile Ser Gly Pro Asn Arg Arg Gln Gly Thr Gln Ala Glu Asn
 1               5                  10                  15

Thr Glu Ser Ala Ser Ser Ser Ser Val Thr Asn Pro Pro Leu Gln Arg
            20                  25                  30

Gly Glu Gly Arg Arg Leu Arg Arg Gln Asp Ala Leu Pro Thr Asp Ile
        35                  40                  45

Arg Tyr Asn Ala Asn Gln Thr Ala Thr Ser Pro Gln Asn Ala Arg Ala
    50                  55                  60

Ala Gly Arg Tyr Glu Ser Gly Ala Ser Ser Ser Gly Ala Asn Asp Thr
65                  70                  75                  80

Pro Gln Ala Glu Gly Ser Met Pro Ser Ser Ser Ala Leu Leu Gln Phe
                85                  90                  95

Arg Leu Ala Gly Gly Arg Asn His Ser Glu Leu Glu Asn Phe His Thr
            100                 105                 110

Met Met Leu Asn Ser Pro Lys Ala Ser Arg Gly Asp Ala Ile Pro Glu
        115                 120                 125

Lys Pro Glu Ala Ile Pro Lys Arg Leu Leu Glu Lys Met Glu Pro Ile
    130                 135                 140

Asn Leu Ala Gln Leu Ala Leu Arg Asp Lys Asp Leu His Glu Tyr Ala
145                 150                 155                 160

Val Met Val Cys Asn Gln Val Lys Lys Gly Glu Gly Pro Asn Ser Asn
                165                 170                 175

Ile Thr Gln Gly Asp Ile Lys Leu Leu Pro Leu Phe Ala Lys Ala Glu
            180                 185                 190

Asn Thr Arg Asn Pro Gly Leu Asn Leu His Thr Phe Lys Ser His Lys
        195                 200                 205

Asp Cys Tyr Gln Ala Ile Lys Glu Gln Asn Arg Asp Ile Gln Lys Asn
    210                 215                 220

Lys Gln Ser Leu Ser Met Arg Val Val Tyr Pro Pro Phe Lys Lys Met
225                 230                 235                 240

Pro Asp His His Ile Ala Leu Asp Ile Gln Leu Arg Tyr Gly His Arg
                245                 250                 255

Pro Ser Ile Val Gly Phe Glu Ser Ala Pro Gly Asn Ile Ile Asp Ala
            260                 265                 270
```

```
Ala Glu Arg Glu Ile Leu Ser Ala Leu Gly Asn Val Lys Ile Lys Met
        275                 280                 285

Val Gly Asn Phe Leu Gln Tyr Ser Lys Thr Asp Cys Thr Met Phe Ala
    290                 295                 300

Leu Asn Asn Ala Leu Lys Ala Phe Lys His His Glu Glu Tyr Thr Ala
305                 310                 315                 320

Arg Leu His Asn Gly Glu Lys Gln Val Pro Ile Pro Ala Thr Phe Leu
                325                 330                 335

Lys His Ala Gln Ser Lys Ser Leu Val Glu Asn His Pro Glu Lys Asp
            340                 345                 350

Thr Thr Val Thr Lys Asp Gln Gly Gly Leu His Met Glu Thr Leu Leu
        355                 360                 365

His Arg Asn Arg Ala Tyr Arg Ala Gln Arg Ser Ala Gly Gln His Val
    370                 375                 380

Thr Ser Ile Glu Gly Phe Arg Met Gln Glu Ile Lys Arg Ala Gly Asp
385                 390                 395                 400

Phe Leu Ala Ala Asn Arg Val Arg Ala Lys Pro
                405                 410
```

The DNA molecule of *ORF6* from the *Pseudomonas syringae* pv. syringae B728a EEL has a nucleotide sequence (SEQ. ID. No. 33) as follows:

```
atgacgctgg aacggattga acagcaaaat acgctgtttg tttatctgtg cgtgggcacg 60
ctttctactc cagccagcag cacacttctg agcgatattc tggccgccaa cctctttcat 120
tatgggtcca gcgatggggc ggccttcggg ctggacgaaa aaaataatga agtgctgctt 180
tttcagcggt ttgatccgtt acggattgat gaggatcact ttgtcagcgc ctgcgttcag 240
atgatcgaag tggcgaaaat atggcgggca aagttactgc atggccattc tgctccgctc 300
gcctcctcaa ccaggctgac gaaagccggt ttaatgctaa ccatggcggg gactattcga 360
tga                                                               363
```

The protein or polypeptide encoded by *Psy* B728a EEL *ORF6* has an amino acid sequence (SEQ. ID. No. 34) as follows:

```
Met Thr Leu Glu Arg Ile Glu Gln Gln Asn Thr Leu Phe Val Tyr Leu
 1               5                  10                  15

Cys Val Gly Thr Leu Ser Thr Pro Ala Ser Ser Thr Leu Leu Ser Asp
            20                  25                  30

Ile Leu Ala Ala Asn Leu Phe His Tyr Gly Ser Ser Asp Gly Ala Ala
        35                  40                  45

Phe Gly Leu Asp Glu Lys Asn Asn Glu Val Leu Leu Phe Gln Arg Phe
    50                  55                  60

Asp Pro Leu Arg Ile Asp Glu Asp His Phe Val Ser Ala Cys Val Gln
65                  70                  75                  80

Met Ile Glu Val Ala Lys Ile Trp Arg Ala Lys Leu Leu His Gly His
                85                  90                  95
```

```
Ser Ala Pro Leu Ala Ser Ser Thr Arg Leu Thr Lys Ala Gly Leu Met
            100                 105                 110

Leu Thr Met Ala Gly Thr Ile Arg
        115                 120
```

The EEL of *Pseudomonas syringae* pv. syringae 61 contains a number of ORFs. One of the open reading frames encodes the outer membrane protein HopPsyA. The DNA molecule which encodes HopPsyA has a nucleotide sequence (SEQ. ID. No. 35) as follows:

```
gtgaacccta tccatgcacg cttctccagc gtagaagcgc tcagacattc aaacgttgat 60
attcaggcaa tcaaatccga gggtcagttg gaagtcaacg gcaagcgtta cgagattcgt 120
gcggccgctg acggctcaat cgcggtcctc agacccgatc aacagtccaa agcagacaag 180
ttcttcaaag gcgcagcgca tcttattggc ggacaaagcc agcgtgccca aatagcccag 240
gtactcaacg agaaagcggc ggcagttcca cgcctggaca gaatgttggg cagacgcttc 300
gatctggaga agggcggaag tagcgctgtg ggcgccgcaa tcaaggctgc cgacagccga 360
ctgacatcaa aacagacatt tgccagcttc cagcaatggg ctgaaaaagc tgaggcgctc 420
gggcgatacc gaaatcggta tctacatgat ctacaagagg gacacgccag acacaacgcc 480
tatgaatgcg gcagagtcaa gaacattacc tggaaacgct acaggctctc gataacaaga 540
aaaaccttat catacgcccc gcagatccat gatgatcggg aagaggaaga gcttgatctg 600
ggccgataca tcgctgaaga cagaaatgcc agaaccggct tttttagaat ggttcctaaa 660
gaccaacgcg cacctgagac aaactcggga cgacttacca ttggtgtaga acctaaatat 720
ggagcgcagt tggccctcgc aatggcaacc ctgatggaca agcacaaatc tgtgacacaa 780
ggtaaagtcg tcggtccggc aaaatatggc cagcaaactg actctgccat tctttacata 840
aatggtgatc ttgcaaaagc agtaaaactg ggcgaaaagc tgaaaaagct gagcggtatc 900
cctcctgaag gattcgtcga acatacaccg ctaagcatgc agtcgacggg tctcggtctt 960
tcttatgccg agtcggttga agggcagcct tccagccacg gacaggcgag aacacacgtt 1020
atcatggatg ccttgaaagg ccagggcccc atggagaaca gactcaaaat ggcgctggca 1080
gaaagaggct atgacccgga aaatccggcg ctcagggcgc gaaactga              1128
```

HopPsyA has an amino acid sequence (SEQ. ID. No. 36) as follows:

```
Val Asn Pro Ile His Ala Arg Phe Ser Ser Val Glu Ala Leu Arg His
  1               5                  10                  15

Ser Asn Val Asp Ile Gln Ala Ile Lys Ser Glu Gly Gln Leu Glu Val
             20                  25                  30

Asn Gly Lys Arg Tyr Glu Ile Arg Ala Ala Ala Asp Gly Ser Ile Ala
         35                  40                  45

Val Leu Arg Pro Asp Gln Gln Ser Lys Ala Asp Lys Phe Phe Lys Gly
     50                  55                  60

Ala Ala His Leu Ile Gly Gly Gln Ser Gln Arg Ala Gln Ile Ala Gln
 65                  70                  75                  80

Val Leu Asn Glu Lys Ala Ala Ala Val Pro Arg Leu Asp Arg Met Leu
                 85                  90                  95

Gly Arg Arg Phe Asp Leu Glu Lys Gly Gly Ser Ser Ala Val Gly Ala
            100                 105                 110

Ala Ile Lys Ala Ala Asp Ser Arg Leu Thr Ser Lys Gln Thr Phe Ala
        115                 120                 125
```

```
Ser Phe Gln Gln Trp Ala Glu Lys Ala Glu Ala Leu Gly Arg Tyr Arg
    130                 135                 140

Asn Arg Tyr Leu His Asp Leu Gln Glu Gly His Ala Arg His Asn Ala
145                 150                 155                 160

Tyr Glu Cys Gly Arg Val Lys Asn Ile Thr Trp Lys Arg Tyr Arg Leu
                165                 170                 175

Ser Ile Thr Arg Lys Thr Leu Ser Tyr Ala Pro Gln Ile His Asp Asp
            180                 185                 190

Arg Glu Glu Glu Glu Leu Asp Leu Gly Arg Tyr Ile Ala Glu Asp Arg
        195                 200                 205

Asn Ala Arg Thr Gly Phe Phe Arg Met Val Pro Lys Asp Gln Arg Ala
    210                 215                 220

Pro Glu Thr Asn Ser Gly Arg Leu Thr Ile Gly Val Glu Pro Lys Tyr
225                 230                 235                 240

Gly Ala Gln Leu Ala Leu Ala Met Ala Thr Leu Met Asp Lys His Lys
                245                 250                 255

Ser Val Thr Gln Gly Lys Val Val Gly Pro Ala Lys Tyr Gly Gln Gln
            260                 265                 270

Thr Asp Ser Ala Ile Leu Tyr Ile Asn Gly Asp Leu Ala Lys Ala Val
        275                 280                 285

Lys Leu Gly Glu Lys Leu Lys Lys Leu Ser Gly Ile Pro Pro Glu Gly
    290                 295                 300

Phe Val Glu His Thr Pro Leu Ser Met Gln Ser Thr Gly Leu Gly Leu
305                 310                 315                 320

Ser Tyr Ala Glu Ser Val Glu Gly Gln Pro Ser Ser His Gly Gln Ala
                325                 330                 335

Arg Thr His Val Ile Met Asp Ala Leu Lys Gly Gln Gly Pro Met Glu
            340                 345                 350

Asn Arg Leu Lys Met Ala Leu Ala Glu Arg Gly Tyr Asp Pro Glu Asn
        355                 360                 365

Pro Ala Leu Arg Ala Arg Asn
    370                 375
```

The remaining open reading frame, designated *shcA*, is a DNA molecule having a nucleotide sequence (SEQ. ID. No. 37) as follows:

```
atggagatgc ccgccttggc gtttgacgat aagggtgcgt gcaacatgat catcgacaag 60
gcattcgctc tgacgctgtt gcgcgacgac acgcatcaac gtttgttgct gattggtctg 120
cttgagccac acgaggatct acccttgcag cgcctgttgg ctggcgctct caaccccctt 180
gtgaatgccg gccccggcat tggctgggat gagcaaagcg gcctgtacca cgcttaccaa 240
agcatcccgc gggaaaaagt cagcgtggag atgctgaagc tcgaaattgc aggattggtc 300
gaatggatga agtgttggcg agaagcccgc acgtga                          336
```

The encoded protein or polypeptide, ShcA, has an amino acid sequence (SEQ. ID. No. 38) as follows:

```
Met Glu Met Pro Ala Leu Ala Phe Asp Asp Lys Gly Ala Cys Asn Met
 1               5                  10                  15

Ile Ile Asp Lys Ala Phe Ala Leu Thr Leu Leu Arg Asp Asp Thr His
            20                  25                  30

Gln Arg Leu Leu Leu Ile Gly Leu Leu Glu Pro His Glu Asp Leu Pro
        35                  40                  45

Leu Gln Arg Leu Leu Ala Gly Ala Leu Asn Pro Leu Val Asn Ala Gly
    50                  55                  60

Pro Gly Ile Gly Trp Asp Glu Gln Ser Gly Leu Tyr His Ala Tyr Gln
65                  70                  75                  80

Ser Ile Pro Arg Glu Lys Val Ser Val Glu Met Leu Lys Leu Glu Ile
                85                  90                  95

Ala Gly Leu Val Glu Trp Met Lys Cys Trp Arg Glu Ala Arg Thr
            100                 105                 110
```

In addition to the above DNA molecules and proteins or polypeptides, the present invention also relates to homologs of various DNA molecules of the present invention which have been isolated from other *Pseudomonas syringae* pathovars. For example, a number of AvrPphE , AvrPphF, and HopPsyA homologs have been identified from *Pseudomonas syringae* pathovars.

The DNA molecule from *Pseudomonas syringae* pv. *angulata* which encodes an AvrPphE homolog has a nucleotide sequence (SEQ. ID. No. 39) as follows:

```
atgagaattc acagtgctgg tcacagcctg cctgcgccag gccctagcgt ggaaaccact 60
gaaaaggctg ttcaatcatc atcggcccag aaccccgctt cttacagttc acaaacagaa 120
cgtcctgaag ccggttcgac tcaagtgcga ctgaactacc cttactcatc agtcaagaca 180
cgcttgccac ccgtttcttc tacagggcag gccatttctg ccacgccatc ttcattgccc 240
ggttacctgc tgttacgtcg gctcgaccga cgtccactgg atgaagacag tatcaaggct 300
ctggttccgg cagacgaagc ggtgcgtgaa gcacgccgcg cgttgccctt cggcaggggc 360
aacattgatg tggatgcaca acgtacccac ctgcaaagcg gcgctcgcgc agtcgctgca 420
aagcgcttga gaaaagatgc cgagcgcgct ggccatgagc cgatgcccgg gaatgatgag 480
atgaactggc atgttcttgt cgccatgtca gggcaggtgt ttggcgctgg caactgtggc 540
gaacatgctc gtatagcaag cttcgcttac ggggccctgg ctcaggaaag cgggcgtagt 600
ccccgcgaaa agattcattt ggccgagcag cccggaaaag atcacgtctg ggctgaaacg 660
gataattcca gcgctggctc ttcgcccatc gtcatggacc cgtggtctaa cggcgcagcc 720
attttggcgg aggacagccg gtttgccaaa gatcgcagta cggtagagcg aacatattca 780
ttcacccttg caatggcagc tgaagccggc aaggttacgc gtgaaaccgc cgagaacgtt 840
ctgacccaca cgacaagccg tctgcagaaa cgtcttgctg atcagttgcc gaacgtctca 900
ccgcttgaag gaggccgcta tcagcaggaa aagtcggtgc ttgatgaggc gttcgcccga 960
cgagtgagcg acaagttgaa tagtgacgat ccacggcgtg cgttgcagat ggaaattgaa 1020
gctgttggtg ttgcaatgtc gctgggtgcc gaaggcgtca agacggtcgc ccgacaggcg 1080
ccaaaggtgg tcaggcaagc cagaagcgtc gcgtcgtcta aaggcatgcc tccacgaaga 1140
taa                                                               1143
```

The amino acid sequence (SEQ. ID. No. 40) for the AvrPphE homolog of *Pseudomonas syringae* pv. *angulata* is as follows:

```
Met Arg Ile His Ser Ala Gly His Ser Leu Pro Ala Pro Gly Pro Ser
 1               5                  10                  15

Val Glu Thr Thr Glu Lys Ala Val Gln Ser Ser Ser Ala Gln Asn Pro
            20                  25                  30

Ala Ser Tyr Ser Ser Gln Thr Glu Arg Pro Glu Ala Gly Ser Thr Gln
        35                  40                  45

Val Arg Leu Asn Tyr Pro Tyr Ser Ser Val Lys Thr Arg Leu Pro Pro
    50                  55                  60

Val Ser Ser Thr Gly Gln Ala Ile Ser Ala Thr Pro Ser Ser Leu Pro
65                  70                  75                  80

Gly Tyr Leu Leu Leu Arg Arg Leu Asp Arg Arg Pro Leu Asp Glu Asp
                85                  90                  95

Ser Ile Lys Ala Leu Val Pro Ala Asp Glu Ala Val Arg Glu Ala Arg
            100                 105                 110

Arg Ala Leu Pro Phe Gly Arg Gly Asn Ile Asp Val Asp Ala Gln Arg
        115                 120                 125

Thr His Leu Gln Ser Gly Ala Arg Ala Val Ala Ala Lys Arg Leu Arg
    130                 135                 140

Lys Asp Ala Glu Arg Ala Gly His Glu Pro Met Pro Gly Asn Asp Glu
145                 150                 155                 160

Met Asn Trp His Val Leu Val Ala Met Ser Gly Gln Val Phe Gly Ala
                165                 170                 175

Gly Asn Cys Gly Glu His Ala Arg Ile Ala Ser Phe Ala Tyr Gly Ala
            180                 185                 190

Leu Ala Gln Glu Ser Gly Arg Ser Pro Arg Glu Lys Ile His Leu Ala
        195                 200                 205

Glu Gln Pro Gly Lys Asp His Val Trp Ala Glu Thr Asp Asn Ser Ser
    210                 215                 220

Ala Gly Ser Ser Pro Ile Val Met Asp Pro Trp Ser Asn Gly Ala Ala
225                 230                 235                 240

Ile Leu Ala Glu Asp Ser Arg Phe Ala Lys Asp Arg Ser Thr Val Glu
                245                 250                 255

Arg Thr Tyr Ser Phe Thr Leu Ala Met Ala Ala Glu Ala Gly Lys Val
            260                 265                 270

Thr Arg Glu Thr Ala Glu Asn Val Leu Thr His Thr Thr Ser Arg Leu
        275                 280                 285

Gln Lys Arg Leu Ala Asp Gln Leu Pro Asn Val Ser Pro Leu Glu Gly
    290                 295                 300

Gly Arg Tyr Gln Gln Glu Lys Ser Val Leu Asp Glu Ala Phe Ala Arg
305                 310                 315                 320
```

```
Arg Val Ser Asp Lys Leu Asn Ser Asp Asp Pro Arg Arg Ala Leu Gln
                325                 330                 335

Met Glu Ile Glu Ala Val Gly Val Ala Met Ser Leu Gly Ala Glu Gly
            340                 345                 350

Val Lys Thr Val Ala Arg Gln Ala Pro Lys Val Val Arg Gln Ala Arg
        355                 360                 365

Ser Val Ala Ser Ser Lys Gly Met Pro Pro Arg Arg
    370                 375                 380
```

This protein or polypeptide has GC content of about 57 percent, an estimated isoelectric point of about 9.5, and an estimated molecular weight of about 41 kDa.

The DNA molecule from *Pseudomonas syringae* pv. *glycinea* which encodes an AvrPphE homolog has a nucleotide sequence (SEQ. ID. No. 41) as follows:

```
atgagaattc acagtgctgg tcacagcctg cccgcgccag gccctagcgt ggaaaccact 60
gaaaaggctg ttcaatcatc atcggcccag aaccccgctt cttgcagttc acaaacagaa 120
cgtcctgaag ccggttcgac tcaagtgcga ccgaactacc cttactcatc agtcaagaca 180
cgcttgccac ccgtttcttc cacagggcag gccatttctg acacgccatc ttcattgtcc 240
ggttacctgc tgttacgtcg gctcgaccga cgtccactgg atgaagacag tatcaaggct 300
ctggttccgg cagacgaagc gttgcgtgaa gcacgccgcg cgttgccctt cggcaggggc 360
aacattgatg tggatgcaca acgtacccac ctgcaaagcg gcgctcgcgc agtcgctgca 420
aagcgcttga gaaaagatgc cgagcgcgct ggccatgagc cgatgcccga gaatgatgag 480
atgaactggc atgttcttgt cgccatgtca gggcaggtgt ttggcgctgg caactgtggc 540
gaacatgctc gtatagcaag cttcgcttac ggggccctgg ctcaggaaag cgggcgtagt 600
ccccgcgaaa agattcattt ggccgagcag cccggaaaag atcacgtctg ggctgaaacg 660
gataattcca gcgctggctc ttcgcccatc gtcatggacc cgtggtctaa cggcgtagcc 720
attttggcgg aggacagccg gtttgccaaa gatcgcagtg cggtagagcg aacatattca 780
ttcacccttg caatggcagc tgaagccggc aaggttgcgc gtgaaaccgc cgagaacgtt 840
ctgacccaca cgacaagccg tctgcagaaa cgtcttgctg atcagttgcc gaacgtctca 900
ccgcttgaag gaggccgcta tcagccggaa aagtcggtgc ttgatgaggc gttcgcccga 960
cgagtgagcg acaagttgaa tagtgacgat ccacggcgtg cgttgcagat ggaaattgaa 1020
gctgttggtg ttgcaatgtc gctgggtgcc gaaggcgtca agacggtcgc ccgacaggcg 1080
ccaaaggtgg tcaggcaagc cagaagcgtc gcgtcgtcta aaggcatgcc tccacgaaga 1140
taa                                                              1143
```

The amino acid sequence (SEQ. ID. No. 42) for the AvrPphE homolog of *Pseudomonas syringae* pv. *glycinea* is as follows:

```
Met Arg Ile His Ser Ala Gly His Ser Leu Pro Ala Pro Gly Pro Ser
  1               5                  10                  15

Val Glu Thr Thr Glu Lys Ala Val Gln Ser Ser Ser Ala Gln Asn Pro
             20                  25                  30

Ala Ser Cys Ser Ser Gln Thr Glu Arg Pro Glu Ala Gly Ser Thr Gln
         35                  40                  45

Val Arg Pro Asn Tyr Pro Tyr Ser Ser Val Lys Thr Arg Leu Pro Pro
     50                  55                  60

Val Ser Ser Thr Gly Gln Ala Ile Ser Asp Thr Pro Ser Ser Leu Ser
 65                  70                  75                  80
```

```
Gly Tyr Leu Leu Leu Arg Arg Leu Asp Arg Arg Pro Leu Asp Glu Asp
                    85                  90                  95

Ser Ile Lys Ala Leu Val Pro Ala Asp Glu Ala Leu Arg Glu Ala Arg
            100                 105                 110

Arg Ala Leu Pro Phe Gly Arg Gly Asn Ile Asp Val Asp Ala Gln Arg
        115                 120                 125

Thr His Leu Gln Ser Gly Ala Arg Ala Val Ala Ala Lys Arg Leu Arg
    130                 135                 140

Lys Asp Ala Glu Arg Ala Gly His Glu Pro Met Pro Glu Asn Asp Glu
145                 150                 155                 160

Met Asn Trp His Val Leu Val Ala Met Ser Gly Gln Val Phe Gly Ala
                165                 170                 175

Gly Asn Cys Gly Glu His Ala Arg Ile Ala Ser Phe Ala Tyr Gly Ala
            180                 185                 190

Leu Ala Gln Glu Ser Gly Arg Ser Pro Arg Glu Lys Ile His Leu Ala
        195                 200                 205

Glu Gln Pro Gly Lys Asp His Val Trp Ala Glu Thr Asp Asn Ser Ser
    210                 215                 220

Ala Gly Ser Ser Pro Ile Val Met Asp Pro Trp Ser Asn Gly Val Ala
225                 230                 235                 240

Ile Leu Ala Glu Asp Ser Arg Phe Ala Lys Asp Arg Ser Ala Val Glu
                245                 250                 255

Arg Thr Tyr Ser Phe Thr Leu Ala Met Ala Ala Glu Ala Gly Lys Val
            260                 265                 270

Ala Arg Glu Thr Ala Glu Asn Val Leu Thr His Thr Thr Ser Arg Leu
        275                 280                 285

Gln Lys Arg Leu Ala Asp Gln Leu Pro Asn Val Ser Pro Leu Glu Gly
    290                 295                 300

Gly Arg Tyr Gln Pro Glu Lys Ser Val Leu Asp Glu Ala Phe Ala Arg
305                 310                 315                 320

Arg Val Ser Asp Lys Leu Asn Ser Asp Asp Pro Arg Arg Ala Leu Gln
                325                 330                 335

Met Glu Ile Glu Ala Val Gly Val Ala Met Ser Leu Gly Ala Glu Gly
            340                 345                 350

Val Lys Thr Val Ala Arg Gln Ala Pro Lys Val Val Arg Gln Ala Arg
        355                 360                 365

Ser Val Ala Ser Ser Lys Gly Met Pro Pro Arg Arg
    370                 375                 380
```

This protein or polypeptide has GC content of about 57 percent, an estimated isoelectric point of about 9.1, and an estimated molecular weight of about 41 kDa.

The DNA molecule from *Pseudomonas syringae* pv. *tabaci* which encodes an AvrPphE homolog has a nucleotide sequence (SEQ. ID. No. 43) as follows:

```
atgagaattc acagtgctgg tcacagcctg cctgcgccag gccctagcgt ggaaaccact 60
gaaaaggctg ttcaatcatc atcggcccag aaccccgctt cttgcagttc acaaacagaa 120
cgtcctgaag ccggttcgac tcaagtgcga ccgaactacc cttactcatc agtcaagaca 180
cgcttgccac ccgtttcttc tacagggcag gccatttctg acacgccatc ttcattgccc 240
ggttacctgc tgttacgtcg gctcgaccga cgtccactgg atgaagacag tatcaaggct 300
ctggttccgg cagacgaagc ggtgcgtgaa gcacgccgcg cgttgccctt cggcaggggc 360
aacattgatg tggatgcaca acgtacccac ctgcaaagcg gcgctcgcgc agtcgctgca 420
aagcgcttga gaaaagatgc cgagcgcgct ggccatgagc cgatgcccgg gaatgatgag 480
atgaactggc atgttcttgt cgccatgtca gggcaggtgt ttggcgctgg caactgtggc 540
gaacatgctc gtatagcaag cttcgcttac ggggccctgg ctcaggaaag cgggcgtagt 600
ccccgcgaaa agattcattt ggccgagcag cccggaaaag atcacgtctg ggctgaaacg 660
gataattcca gcgctggctc ttcgcccatc gtcatggacc cgtggtctaa cggcgcagcc 720
attttggcgg aggacagccg gtttgccaaa gatcgcagtg cggtagagcg aacatattca 780
ttcacccttg caatggcagc tgaagccggc aaggttacgc gtgaaactgc cgagaacgtt 840
ctgacccaca cgacaagccg tctgcagaaa cgtcttgctg atcagttgcc gaacgtctca 900
ccgcttgaag gaggccgcta tcagcaggaa aagtcggtgc ttgatgaggc gttcgcccga 960
cgagtgagcg acaagttgaa tagtgacgat ccacggcgtg cgttgcagat ggaaattgaa 1020
gctgttggtg ttgcaatgtc gctgggtgcc gaaggcgtca agacggtcgc ccgacaggcg 1080
ccaaaggtgg tcaggcaagc cagaagcgtc gcgtcgtcta aaggcatgcc tccacgaaga 1140
taa                                                              1143
```

The amino acid sequence (SEQ. ID. No. 44) for the AvrPphE homolog of *Pseudomonas syringae* pv. *tabaci* is as follows:

```
Met Arg Ile His Ser Ala Gly His Ser Leu Pro Ala Pro Gly Pro Ser
  1               5                  10                  15

Val Glu Thr Thr Glu Lys Ala Val Gln Ser Ser Ser Ala Gln Asn Pro
             20                  25                  30

Ala Ser Cys Ser Ser Gln Thr Glu Arg Pro Glu Ala Gly Ser Thr Gln
         35                  40                  45

Val Arg Pro Asn Tyr Pro Tyr Ser Ser Val Lys Thr Arg Leu Pro Pro
     50                  55                  60

Val Ser Ser Thr Gly Gln Ala Ile Ser Asp Thr Pro Ser Ser Leu Pro
 65                  70                  75                  80

Gly Tyr Leu Leu Leu Arg Arg Leu Asp Arg Arg Pro Leu Asp Glu Asp
                 85                  90                  95

Ser Ile Lys Ala Leu Val Pro Ala Asp Glu Ala Val Arg Glu Ala Arg
            100                 105                 110

Arg Ala Leu Pro Phe Gly Arg Gly Asn Ile Asp Val Asp Ala Gln Arg
        115                 120                 125

Thr His Leu Gln Ser Gly Ala Arg Ala Val Ala Ala Lys Arg Leu Arg
    130                 135                 140

Lys Asp Ala Glu Arg Ala Gly His Glu Pro Met Pro Gly Asn Asp Glu
145                 150                 155                 160
```

```
Met Asn Trp His Val Leu Val Ala Met Ser Gly Gln Val Phe Gly Ala
                165                 170                 175

Gly Asn Cys Gly Glu His Ala Arg Ile Ala Ser Phe Ala Tyr Gly Ala
            180                 185                 190

Leu Ala Gln Glu Ser Gly Arg Ser Pro Arg Glu Lys Ile His Leu Ala
        195                 200                 205

Glu Gln Pro Gly Lys Asp His Val Trp Ala Glu Thr Asp Asn Ser Ser
    210                 215                 220

Ala Gly Ser Ser Pro Ile Val Met Asp Pro Trp Ser Asn Gly Ala Ala
225                 230                 235                 240

Ile Leu Ala Glu Asp Ser Arg Phe Ala Lys Asp Arg Ser Ala Val Glu
                245                 250                 255

Arg Thr Tyr Ser Phe Thr Leu Ala Met Ala Ala Glu Ala Gly Lys Val
            260                 265                 270

Thr Arg Glu Thr Ala Glu Asn Val Leu Thr His Thr Thr Ser Arg Leu
        275                 280                 285

Gln Lys Arg Leu Ala Asp Gln Leu Pro Asn Val Ser Pro Leu Glu Gly
    290                 295                 300

Gly Arg Tyr Gln Gln Glu Lys Ser Val Leu Asp Glu Ala Phe Ala Arg
305                 310                 315                 320

Arg Val Ser Asp Lys Leu Asn Ser Asp Asp Pro Arg Arg Ala Leu Gln
                325                 330                 335

Met Glu Ile Glu Ala Val Gly Val Ala Met Ser Leu Gly Ala Glu Gly
            340                 345                 350

Val Lys Thr Val Ala Arg Gln Ala Pro Lys Val Val Arg Gln Ala Arg
        355                 360                 365

Ser Val Ala Ser Ser Lys Gly Met Pro Pro Arg Arg
    370                 375                 380
```

This protein or polypeptide has GC content of about 57 percent, an estimated isoelectric point of about 9.3, and an estimated molecular weight of about 41 kDa.

Another DNA molecule from *Pseudomonas syringae* pv. *tabaci* which encodes a AvrPphE homolog has a nucleotide sequence (SEQ. ID. No. 45) as follows:

```
atgagaattc acagtgctgg tcacagcctg cctgcgccag gccctagcgt ggaaaccact 60
gaaaaggctg ttcaatcatc atcggcccag aaccccgctt cttgcagttc acaaacagaa 120
cgtcctgaag ccggttcgac tcaagtgcga ccgaactacc cttactcatc agtcaagaca 180
cgcttgccac ccgtttcttc tacagggcag gccatttctg acacgccatc ttcattgccc 240
ggttacctgc tgttacgtcg gctcgaccga cgtccactgg atgaagacag tatcaaggct 300
ctggttccgg cagacgaagc ggtgcgtgaa gcacgccgcg cgttgccctt cggcaggggc 360
aacattgatg tggatgcaca acgtacccac ctgcaaagcg gcgctcgcgc agtcgctgca 420
aagcgcttga gaaaagatgc cgagcgcgct ggccatgagc cgatgcccgg gaatgatgag 480
atgaactggc atgttcttgt cgccatgtca gggcaggtgt ttggcgctgg caactgtggc 540
gaacatgctc gtatagcaag cttcgcttac ggggccctgg ctcaggaaag cgggcgtagt 600
ccccgcgaaa agattcattt ggccgagcag cccggaaaag atcacgtctg ggctgaaacg 660
gataattcca gcgctggctc ttcgcccatc gtcatggacc cgtggtctaa cggcgcagcc 720
attttggcgg aggacagccg gtttgccaaa gatcgcagtg cggtagagcg aacatattca 780
```

```
ttcacccttg caatggcagc tgaagccggc aaggttacgc gtgaaactgc cgagaacgtt 840
ctgacccaca cgacaagccg tctgcagaaa cgtcttgctg atcagttgcc gaacgtctca 900
ccgcttgaag gaggccgcta tcagcaggaa aagtcggtgc ttgatgaggc gttcgcccga 960
cgagtgagcg acaagttgaa tagtgacgat ccacggcgtg cgttgcagat ggaaattgaa 1020
gctgttggtg ttgcaatgtc gctgggtgcc gaaggcgtca agacggtcgc ccgacaggcg 1080
ccaaaggtgg tcaggcaagc cagaagcgtc gcgtcgtcta aaggcatgcc tccacgaaga 1140
taa                                                               1143
```

The encoded AvrPphE homolog has an amino acid sequence according to SEQ. ID. No. 46 as follows:

```
Met Arg Ile His Ser Ala Gly His Ser Leu Pro Ala Pro Gly Pro Ser
 1               5                  10                  15

Val Glu Thr Thr Glu Lys Ala Val Gln Ser Ser Ser Ala Gln Asn Pro
            20                  25                  30

Ala Ser Cys Ser Ser Gln Thr Glu Arg Pro Glu Ala Gly Ser Thr Gln
        35                  40                  45

Val Arg Pro Asn Tyr Pro Tyr Ser Ser Val Lys Thr Arg Leu Pro Pro
    50                  55                  60

Val Ser Ser Thr Gly Gln Ala Ile Ser Asp Thr Pro Ser Ser Leu Pro
65                  70                  75                  80

Gly Tyr Leu Leu Leu Arg Arg Leu Asp Arg Arg Pro Leu Asp Glu Asp
                85                  90                  95

Ser Ile Lys Ala Leu Val Pro Ala Asp Glu Ala Val Arg Glu Ala Arg
            100                 105                 110

Arg Ala Leu Pro Phe Gly Arg Gly Asn Ile Asp Val Asp Ala Gln Arg
        115                 120                 125

Thr His Leu Gln Ser Gly Ala Arg Ala Val Ala Ala Lys Arg Leu Arg
    130                 135                 140

Lys Asp Ala Glu Arg Ala Gly His Glu Pro Met Pro Gly Asn Asp Glu
145                 150                 155                 160

Met Asn Trp His Val Leu Val Ala Met Ser Gly Gln Val Phe Gly Ala
                165                 170                 175

Gly Asn Cys Gly Glu His Ala Arg Ile Ala Ser Phe Ala Tyr Gly Ala
            180                 185                 190

Leu Ala Gln Glu Ser Gly Arg Ser Pro Arg Glu Lys Ile His Leu Ala
        195                 200                 205

Glu Gln Pro Gly Lys Asp His Val Trp Ala Glu Thr Asp Asn Ser Ser
    210                 215                 220

Ala Gly Ser Ser Pro Ile Val Met Asp Pro Trp Ser Asn Gly Ala Ala
225                 230                 235                 240

Ile Leu Ala Glu Asp Ser Arg Phe Ala Lys Asp Arg Ser Ala Val Glu
                245                 250                 255

Arg Thr Tyr Ser Phe Thr Leu Ala Met Ala Ala Glu Ala Gly Lys Val
            260                 265                 270
```

```
Thr Arg Glu Thr Ala Glu Asn Val Leu Thr His Thr Thr Ser Arg Leu
        275                 280                 285

Gln Lys Arg Leu Ala Asp Gln Leu Pro Asn Val Ser Pro Leu Glu Gly
    290                 295                 300

Gly Arg Tyr Gln Gln Glu Lys Ser Val Leu Asp Glu Ala Phe Ala Arg
305                 310                 315                 320

Arg Val Ser Asp Lys Leu Asn Ser Asp Asp Pro Arg Arg Ala Leu Gln
                325                 330                 335

Met Glu Ile Glu Ala Val Gly Val Ala Met Ser Leu Gly Ala Glu Gly
            340                 345                 350

Val Lys Thr Val Ala Arg Gln Ala Pro Lys Val Val Arg Gln Ala Arg
        355                 360                 365

Ser Val Ala Ser Ser Lys Gly Met Pro Pro Arg Arg
    370                 375                 380
```

A DNA molecule from *Pseudomonas syringae* pv. *glycinea* race 4 which encodes an AvrPphE homolog has a nucleotide sequence (SEQ. ID. No. 47) as follows:

```
atgagaattc acagtgctgg tcacagcctg cccgccgcag gccctagcgt ggaaaccact 60
gaaaaggctg ttcaatcatc atcggcccag aaccccgctt cttgcagttc acaaacagaa 120
cgtcctgaag ccggttcgac tcaagtgcga ccgaactacc cttactcatc agtcaagaca 180
cgcttgccac ccgtttcttc cacagggcag gccatttctg acacgccatc ttcattgtcc 240
ggttacctgc tgttacgtcg gctcgaccga cgtccactgg atgaagacag tatcaaggct 300
ctggttccgg cagacgaagc gttgcgtgaa gcacgccgcg cgttgccctt cggcaggggc 360
aacattgatg tggatgcaca acgtacccac ctgcaaagcg gcgctcgcgc agtcgctgca 420
aagcgcttga gaaaagatgc cgagcgcgct ggccatgagc cgatgcccga gaatgatgag 480
atgaactggc atgttcttgt cgccatgtca gggcaggtgt ttggcgctgg caactgtggc 540
gaacatgctc gtatagcaag cttcgcttac ggggccctgg ctcaggaaag cgggcgtagt 600
ccccgcgaaa agattcattt ggccgagcag cccggaaaag atcacgtctg ggctgaaacg 660
gataattcca gcgctggctc ttcgcccatc gtcatggacc cgtggtctaa cggcgtagcc 720
attttggcgg aggacagccg gtttgccaaa gatcgcagtg cggtagagcg aacatattca 780
ttcacccttg caatggcagc tgaagccggc aaggttgcgc gtgaaaccgc cgagaacgtt 840
ctgacccaca cgacaagccg tctgcagaaa cgtcttgctg atcagttgcc gaacgtctca 900
ccgcttgaag gaggccgcta tcagccggaa aagtcggtgc ttgatgaggc gttcgcccga 960
cgagtgagcg acaagttgaa tagtgacgat ccacggcgtg cgttgcagat ggaaattgaa 1020
gctgttggtg ttgcaatgtc gctgggtgcc gaaggcgtca agacggtcgc ccgacaggcg 1080
ccaaaggtgg tcaggcaagc cagaagcgtc gcgtcgtcta aaggcatgcc tccacgaaga 1140
taa                                                              1143
```

The encoded AvrPphE homolog has an amino acid sequence according to SEQ. ID. No. 48 as follows:

```
Met Arg Ile His Ser Ala Gly His Ser Leu Pro Ala Pro Gly Pro Ser
  1               5                  10                  15

Val Glu Thr Thr Glu Lys Ala Val Gln Ser Ser Ser Ala Gln Asn Pro
             20                  25                  30

Ala Ser Cys Ser Ser Gln Thr Glu Arg Pro Glu Ala Gly Ser Thr Gln
         35                  40                  45
```

```
Val Arg Pro Asn Tyr Pro Tyr Ser Ser Val Lys Thr Arg Leu Pro Pro
     50                  55                  60

Val Ser Ser Thr Gly Gln Ala Ile Ser Asp Thr Pro Ser Ser Leu Ser
 65                  70                  75                  80

Gly Tyr Leu Leu Leu Arg Arg Leu Asp Arg Arg Pro Leu Asp Glu Asp
                 85                  90                  95

Ser Ile Lys Ala Leu Val Pro Ala Asp Glu Ala Leu Arg Glu Ala Arg
            100                 105                 110

Arg Ala Leu Pro Phe Gly Arg Gly Asn Ile Asp Val Asp Ala Gln Arg
        115                 120                 125

Thr His Leu Gln Ser Gly Ala Arg Ala Val Ala Ala Lys Arg Leu Arg
    130                 135                 140

Lys Asp Ala Glu Arg Ala Gly His Glu Pro Met Pro Glu Asn Asp Glu
145                 150                 155                 160

Met Asn Trp His Val Leu Val Ala Met Ser Gly Gln Val Phe Gly Ala
                165                 170                 175

Gly Asn Cys Gly Glu His Ala Arg Ile Ala Ser Phe Ala Tyr Gly Ala
            180                 185                 190

Leu Ala Gln Glu Ser Gly Arg Ser Pro Arg Glu Lys Ile His Leu Ala
        195                 200                 205

Glu Gln Pro Gly Lys Asp His Val Trp Ala Glu Thr Asp Asn Ser Ser
    210                 215                 220

Ala Gly Ser Ser Pro Ile Val Met Asp Pro Trp Ser Asn Gly Val Ala
225                 230                 235                 240

Ile Leu Ala Glu Asp Ser Arg Phe Ala Lys Asp Arg Ser Ala Val Glu
                245                 250                 255

Arg Thr Tyr Ser Phe Thr Leu Ala Met Ala Ala Glu Ala Gly Lys Val
            260                 265                 270

Ala Arg Glu Thr Ala Glu Asn Val Leu Thr His Thr Thr Ser Arg Leu
        275                 280                 285

Gln Lys Arg Leu Ala Asp Gln Leu Pro Asn Val Ser Pro Leu Glu Gly
    290                 295                 300

Gly Arg Tyr Gln Pro Glu Lys Ser Val Leu Asp Glu Ala Phe Ala Arg
305                 310                 315                 320

Arg Val Ser Asp Lys Leu Asn Ser Asp Asp Pro Arg Arg Ala Leu Gln
                325                 330                 335

Met Glu Ile Glu Ala Val Gly Val Ala Met Ser Leu Gly Ala Glu Gly
            340                 345                 350

Val Lys Thr Val Ala Arg Gln Ala Pro Lys Val Val Arg Gln Ala Arg
        355                 360                 365

Ser Val Ala Ser Ser Lys Gly Met Pro Pro Arg Arg
    370                 375                 380
```

A DNA molecule from *Pseudomonas syringae* pv. *phaseolicola* strain B130 which encodes AvrPphE has a nucleotide sequence (SEQ. ID. No. 49) as follows:

```
atgagaattc acagtgctgg tcacagcctg cccgcgccag gccctagcgt ggaaaccact 60
gaaaaggctg ttcaatcatc atcggcccag aaccccgctt cttgcagttc acaaacagaa 120
cgtcctgaag ccggttcgac tcaagtgcga ccgaactacc cttactcatc agtcaagaca 180
cgcttgccac ccgtttcttc cacagggcag gccatttctg acacgccatc ttcattgccc 240
ggttacctgc tgttacgtcg gctcgaccga cgtccactgg atgaagacag tatcaaggct 300
ctggttccgg cagacgaagc gttgcgtgaa gcacgccgcg cgttgccctt cggcaggggc 360
aacattgatg tggatgcaca acgtacccac ctgcaaagcg gcgctcgcgc agtcgctgca 420
aagcgcttga gaaaagatgc cgagcgcgct ggccatgagc cgatgcccga gaatgatgag 480
atgaactggc atgttcttgt cgccatgtca gggcaggtgt ttggcgctgg caactgtggc 540
gaacatgctc gtatagcaag cttcgcttac ggggccctgg ctcaggaaag cgggcgtagt 600
ccccgcgaaa agattcattt ggccgagcag cccggaaaag atcacgtctg ggctgaaacg 660
gataattcca gcgctggctc ttcgcccatc gtcatggacc cgtggtctaa cggcgcagcc 720
attttggcgg aggacagccg gtttgccaaa gatcgcagtg cggtagagcg aacatattca 780
ttcacccttg caatggcagc tgaagccggc aaggttgcgc gtgaaaccgc cgagaacgtt 840
ctgacccaca cgacaagccg tctgcagaag cgtcttgctg atcagttgcc gaacgtctca 900
ccgcttgaag gaggccgcta tcagccggaa aagtcggtgc ttgatgaggc gttcgcccga 960
cgagtgagcg acaagttgaa tagtgacgat ccacggcgtg cgttgcagat ggaaattgaa 1020
gctgttggtg ttgcaatgtc gctgggtgcc gaaggcgtca agacggtcgc ccgacaggcg 1080
ccaaaggtgg tcaggcaagc cagaagcgtc gcgtcgtcta aaggcatgcc tccacgaaga 1140
taa                                                              1143
```

The encoded AvrPphE homolog has an amino acid sequence according to SEQ. ID. No. 50 as follows:

```
Met Arg Ile His Ser Ala Gly His Ser Leu Pro Ala Pro Gly Pro Ser
  1               5                  10                  15

Val Glu Thr Thr Glu Lys Ala Val Gln Ser Ser Ser Ala Gln Asn Pro
             20                  25                  30

Ala Ser Cys Ser Ser Gln Thr Glu Arg Pro Glu Ala Gly Ser Thr Gln
         35                  40                  45

Val Arg Pro Asn Tyr Pro Tyr Ser Ser Val Lys Thr Arg Leu Pro Pro
     50                  55                  60

Val Ser Ser Thr Gly Gln Ala Ile Ser Asp Thr Pro Ser Ser Leu Pro
 65                  70                  75                  80

Gly Tyr Leu Leu Leu Arg Arg Leu Asp Arg Arg Pro Leu Asp Glu Asp
                 85                  90                  95

Ser Ile Lys Ala Leu Val Pro Ala Asp Glu Ala Leu Arg Glu Ala Arg
            100                 105                 110

Arg Ala Leu Pro Phe Gly Arg Gly Asn Ile Asp Val Asp Ala Gln Arg
        115                 120                 125

Thr His Leu Gln Ser Gly Ala Arg Ala Val Ala Ala Lys Arg Leu Arg
    130                 135                 140

Lys Asp Ala Glu Arg Ala Gly His Glu Pro Met Pro Glu Asn Asp Glu
145                 150                 155                 160
```

```
Met Asn Trp His Val Leu Val Ala Met Ser Gly Gln Val Phe Gly Ala
                165                 170                 175

Gly Asn Cys Gly Glu His Ala Arg Ile Ala Ser Phe Ala Tyr Gly Ala
            180                 185                 190

Leu Ala Gln Glu Ser Gly Arg Ser Pro Arg Glu Lys Ile His Leu Ala
        195                 200                 205

Glu Gln Pro Gly Lys Asp His Val Trp Ala Glu Thr Asp Asn Ser Ser
    210                 215                 220

Ala Gly Ser Ser Pro Ile Val Met Asp Pro Trp Ser Asn Gly Ala Ala
225                 230                 235                 240

Ile Leu Ala Glu Asp Ser Arg Phe Ala Lys Asp Arg Ser Ala Val Glu
                245                 250                 255

Arg Thr Tyr Ser Phe Thr Leu Ala Met Ala Ala Glu Ala Gly Lys Val
            260                 265                 270

Ala Arg Glu Thr Ala Glu Asn Val Leu Thr His Thr Thr Ser Arg Leu
        275                 280                 285

Gln Lys Arg Leu Ala Asp Gln Leu Pro Asn Val Ser Pro Leu Glu Gly
    290                 295                 300

Gly Arg Tyr Gln Pro Glu Lys Ser Val Leu Asp Glu Ala Phe Ala Arg
305                 310                 315                 320

Arg Val Ser Asp Lys Leu Asn Ser Asp Asp Pro Arg Arg Ala Leu Gln
                325                 330                 335

Met Glu Ile Glu Ala Val Gly Val Ala Met Ser Leu Gly Ala Glu Gly
            340                 345                 350

Val Lys Thr Val Ala Arg Gln Ala Pro Lys Val Val Arg Gln Ala Arg
        355                 360                 365

Ser Val Ala Ser Ser Lys Gly Met Pro Pro Arg Arg
    370                 375                 380
```

A DNA molecule from *Pseudomonas syringae* pv. *angulata* strain Pa9 which encodes an AvrPphE homolog has a nucleotide sequence (SEQ. ID. No. 51) as follows:

```
atgagaattc acagtgctgg tcacagcctg cctgcgccag gccctagcgt ggaaaccact 60
gaaaaggctg ttcaatcatc atcggcccag aaccccgctt cttacagttc acaaacagaa 120
cgtcctgaag ccggttcgac tcaagtgcga ctgaactacc cttactcatc agtcaagaca 180
cgcttgccac ccgtttcttc tacagggcag gccatttctg ccacgccatc ttcattgccc 240
ggttacctgc tgttacgtcg gctcgaccga cgtccactgg atgaagacag tatcaaggct 300
ctggttccgg cagacgaagc ggtgcgtgaa gcacgccgcg cgttgccctt cggcaggggc 360
aacattgatg tggatgcaca acgtacccac ctgcaaagcg gcgctcgcgc agtcgctgca 420
aagcgcttga gaaaagatgc cgagcgcgct ggccatgagc cgatgcccgg gaatgatgag 480
atgaactggc atgttcttgt cgccatgtca gggcaggtgt ttggcgctgg caactgtggc 540
gaacatgctc gtatagcaag cttcgcttac ggggccctgg ctcaggaaag cgggcgtagt 600
ccccgcgaaa agattcattt ggccgagcag cccggaaaag atcacgtctg ggctgaaacg 660
gataattcca gcgctggctc ttcgcccatc gtcatggacc cgtggtctaa cggcgcagcc 720
attttggcgg aggacagccg gtttgccaaa gatcgcagta cggtagagcg aacatattca 780
ttcacccttg caatggcagc tgaagccggc aaggttacgc gtgaaaccgc cgagaacgtt 840
ctgacccaca cgacaagccg tctgcagaaa cgtcttgctg atcagttgcc gaacgtctca 900
```

```
ccgcttgaag gaggccgcta tcagcaggaa aagtcggtgc ttgatgaggc gttcgcccga 960
cgagtgagcg acaagttgaa tagtgacgat ccacggcgtg cgttgcagat ggaaattgaa 1020
gctgttggtg ttgcaatgtc gctgggtgcc gaaggcgtca agacggtcgc ccgacaggcg 1080
ccaaaggtgg tcaggcaagc cagaagcgtc gcgtcgtcta aaggcatgcc tccacgaaga 1140
taa                                                               1143
```

The encoded AvrPphE homolog has an amino acid sequence according to SEQ. ID. No. 52 as follows:

```
Met Arg Ile His Ser Ala Gly His Ser Leu Pro Ala Pro Gly Pro Ser
  1               5                  10                  15

Val Glu Thr Thr Glu Lys Ala Val Gln Ser Ser Ser Ala Gln Asn Pro
             20                  25                  30

Ala Ser Tyr Ser Ser Gln Thr Glu Arg Pro Glu Ala Gly Ser Thr Gln
         35                  40                  45

Val Arg Leu Asn Tyr Pro Tyr Ser Ser Val Lys Thr Arg Leu Pro Pro
     50                  55                  60

Val Ser Ser Thr Gly Gln Ala Ile Ser Ala Thr Pro Ser Ser Leu Pro
 65                  70                  75                  80

Gly Tyr Leu Leu Leu Arg Arg Leu Asp Arg Arg Pro Leu Asp Glu Asp
                 85                  90                  95

Ser Ile Lys Ala Leu Val Pro Ala Asp Glu Ala Val Arg Glu Ala Arg
            100                 105                 110

Arg Ala Leu Pro Phe Gly Arg Gly Asn Ile Asp Val Asp Ala Gln Arg
        115                 120                 125

Thr His Leu Gln Ser Gly Ala Arg Ala Val Ala Ala Lys Arg Leu Arg
    130                 135                 140

Lys Asp Ala Glu Arg Ala Gly His Glu Pro Met Pro Gly Asn Asp Glu
145                 150                 155                 160

Met Asn Trp His Val Leu Val Ala Met Ser Gly Gln Val Phe Gly Ala
                165                 170                 175

Gly Asn Cys Gly Glu His Ala Arg Ile Ala Ser Phe Ala Tyr Gly Ala
            180                 185                 190

Leu Ala Gln Glu Ser Gly Arg Ser Pro Arg Glu Lys Ile His Leu Ala
        195                 200                 205

Glu Gln Pro Gly Lys Asp His Val Trp Ala Glu Thr Asp Asn Ser Ser
    210                 215                 220

Ala Gly Ser Ser Pro Ile Val Met Asp Pro Trp Ser Asn Gly Ala Ala
225                 230                 235                 240

Ile Leu Ala Glu Asp Ser Arg Phe Ala Lys Asp Arg Ser Thr Val Glu
                245                 250                 255

Arg Thr Tyr Ser Phe Thr Leu Ala Met Ala Ala Glu Ala Gly Lys Val
            260                 265                 270

Thr Arg Glu Thr Ala Glu Asn Val Leu Thr His Thr Thr Ser Arg Leu
        275                 280                 285
```

```
Gln Lys Arg Leu Ala Asp Gln Leu Pro Asn Val Ser Pro Leu Glu Gly
    290                 295                 300

Gly Arg Tyr Gln Gln Glu Lys Ser Val Leu Asp Glu Ala Phe Ala Arg
305                 310                 315                 320

Arg Val Ser Asp Lys Leu Asn Ser Asp Asp Pro Arg Arg Ala Leu Gln
                325                 330                 335

Met Glu Ile Glu Ala Val Gly Val Ala Met Ser Leu Gly Ala Glu Gly
            340                 345                 350

Val Lys Thr Val Ala Arg Gln Ala Pro Lys Val Val Arg Gln Ala Arg
        355                 360                 365

Ser Val Ala Ser Ser Lys Gly Met Pro Pro Arg Arg
    370                 375                 380
```

A DNA molecule from *Pseudomonas syringae* pv. *delphinii* strain PDDCC529 which encodes a AvrPphE homolog has a nucleotide sequence (SEQ. ID. No. 53) as follows:

```
atgaaaatac ataacgctgg cccaagcatt ccgatgcccg ctccatcgat tgagagcgct 60
ggcaagactg cgcaatcatc attggctcaa ccgcagagcc aacgagccac ccccgtctcg 120
ccatcagaga cttctgatgc ccgtccgtcc agtgtgcgta cgaactaccc ttattcatca 180
gtcaaaacac ggttgcctcc cgttgcgtct gcagggcagc cactgtccgg gatgccgtct 240
tcattacccg gctacttgct gttacgtcgg cttgaccatc gtccactgga tcaagacggt 300
atcaaaggtt tgattccagc agatgaagcg gtgggtgaag cacgtcgcgc gttgcctttc 360
ggcaggggca atatcgacgt ggatgcgcaa cgctccaact tggaaagcgg agcccgcaca 420
ctcgcggcta ggcgtttgag aaaagatgcc gaggccgcgg gtcacgaacc aatgcctgca 480
aatgaagata tgaactggca tgttcttgtt gcgatgtcag gacaggtttt tggcgcaggt 540
aactgcgggg aacatgcccg catagcgagt ttcgcctacg gtgcactggc tcaggaaaaa 600
gggcggaacg ccgatgagac tattcatttg gctgcgcaac gcggtaaaga ccacgtctgg 660
gctgaaacgg acaattcaag cgctggatct tcaccggttg tcatggatcc gtggtcgaac 720
ggtcctgcca tttttgcgga ggatagtcgg tttgccaaag atcgaagtac ggtagaacga 780
acggattcct tcacgcttgc aactgctgct gaagcaggca agatcacgcg agagacggcc 840
gagaatgctt tgacacaggc gaccagccgt ttgcagaaac gtcttgctga tcagaaaacg 900
caagtctcgc cgcttgcagg agggcgctat cggcaagaaa attcggtgct tgatgacgcg 960
ttcgcccgac gggcaagtgg caagttgagc aacaaggatc cgcggcatgc attacaggtg 1020
gaaatcgagg cggccgcagt tgcaatgtcg ctgggcgccc aaggcgtaaa agcggttgcg 1080
gaacaggccc ggacggtagt tgaacaagcc aggaaggtcg catctcccca aggcacgcct 1140
cagcgagata cgtga                                                  1155
```

The encoded AvrPphE homolog has an amino acid sequence according to SEQ. ID. No. 54 as follows:

```
Met Lys Ile His Asn Ala Gly Pro Ser Ile Pro Met Pro Ala Pro Ser
  1               5                  10                  15

Ile Glu Ser Ala Gly Lys Thr Ala Gln Ser Ser Leu Ala Gln Pro Gln
             20                  25                  30

Ser Gln Arg Ala Thr Pro Val Ser Pro Ser Glu Thr Ser Asp Ala Arg
         35                  40                  45

Pro Ser Ser Val Arg Thr Asn Tyr Pro Tyr Ser Ser Val Lys Thr Arg
     50                  55                  60
```

```
Leu Pro Pro Val Ala Ser Ala Gly Gln Pro Leu Ser Gly Met Pro Ser
 65                  70                  75                  80

Ser Leu Pro Gly Tyr Leu Leu Leu Arg Arg Leu Asp His Arg Pro Leu
                 85                  90                  95

Asp Gln Asp Gly Ile Lys Gly Leu Ile Pro Ala Asp Glu Ala Val Gly
            100                 105                 110

Glu Ala Arg Arg Ala Leu Pro Phe Gly Arg Gly Asn Ile Asp Val Asp
        115                 120                 125

Ala Gln Arg Ser Asn Leu Glu Ser Gly Ala Arg Thr Leu Ala Ala Arg
    130                 135                 140

Arg Leu Arg Lys Asp Ala Glu Ala Ala Gly His Glu Pro Met Pro Ala
145                 150                 155                 160

Asn Glu Asp Met Asn Trp His Val Leu Val Ala Met Ser Gly Gln Val
                165                 170                 175

Phe Gly Ala Gly Asn Cys Gly Glu His Ala Arg Ile Ala Ser Phe Ala
            180                 185                 190

Tyr Gly Ala Leu Ala Gln Glu Lys Gly Arg Asn Ala Asp Glu Thr Ile
        195                 200                 205

His Leu Ala Ala Gln Arg Gly Lys Asp His Val Trp Ala Glu Thr Asp
    210                 215                 220

Asn Ser Ser Ala Gly Ser Ser Pro Val Val Met Asp Pro Trp Ser Asn
225                 230                 235                 240

Gly Pro Ala Ile Phe Ala Glu Asp Ser Arg Phe Ala Lys Asp Arg Ser
                245                 250                 255

Thr Val Glu Arg Thr Asp Ser Phe Thr Leu Ala Thr Ala Ala Glu Ala
            260                 265                 270

Gly Lys Ile Thr Arg Glu Thr Ala Glu Asn Ala Leu Thr Gln Ala Thr
        275                 280                 285

Ser Arg Leu Gln Lys Arg Leu Ala Asp Gln Lys Thr Gln Val Ser Pro
    290                 295                 300

Leu Ala Gly Gly Arg Tyr Arg Gln Glu Asn Ser Val Leu Asp Asp Ala
305                 310                 315                 320

Phe Ala Arg Arg Ala Ser Gly Lys Leu Ser Asn Lys Asp Pro Arg His
                325                 330                 335

Ala Leu Gln Val Glu Ile Glu Ala Ala Ala Val Ala Met Ser Leu Gly
            340                 345                 350

Ala Gln Gly Val Lys Ala Val Ala Glu Gln Ala Arg Thr Val Val Glu
        355                 360                 365

Gln Ala Arg Lys Val Ala Ser Pro Gln Gly Thr Pro Gln Arg Asp Thr
    370                 375                 380
```

A DNA molecule from *Pseudomonas syringae* pv. *delphinii* strain PDDCC529 which encodes a homolog of *P. syringae* pv. tomato DC3000 EEL *ORF2* has a nucleotide sequence (SEQ. ID. No. 55) as follows:

```
gtggttgagc gaaccggcac tgcatatcga aggcgtggag cagcctgctc gcgtatcacg 60
agccaaaatc aggtccgacg acgctttgga attacggtga atcagatgca aaagacgtcc 120
ctattggctt tggcctttgc aatcctggca gggtgtgggg gttcggggca ggcgccgggg 180
agtgatattc agggtgccca ggcagagatg aaaacaccca ttaaagtaga tctggatgcc 240
tacacctcaa aaaaacttga tgctgtgttg gaagctcggg ccaataaaag ctatgtgaat 300
aaaggtcaac tgatcgacct tgtgtcaggg gcgtttttgg gaacaccgta ccgctcaaac 360
atgttggtgg gcacagagga aatacctgaa cagttagtca tcgactttag aggtctggat 420
tgttttgctt atctggatta cgtagaggcg ttgcgaagat caacatcgca gcaggatttt 480
gtgaggaatc tcgttcaggt tcgttacaag ggtggtgatg ttgacttttt gaatcgcaag 540
cactttttca cggattgggc ttatggcact acacaccccgg tggcggatga catcaccacg 600
cagataagcc ccggtgcggt aagtgtcaga aaacgcctta atgaaagggc caaaggcaaa 660
gtctatctgc caggtttgcc tgtggttgag cgcagcatga cctatatccc gagccgcctt 720
gtcgacagtc aggtggtaag ccacttgcgc acaggtgatt acatcggcat ttacaccccg 780
cttcccgggc tggatgtgac gcacgtcggt ttctttatca tgacggataa aggccctgtc 840
ttgcgaaatg catcttcacg aaaagaaaac agaaaggtaa tggatttgcc ttttctggac 900
tatgtatcgg aaaagccagg gattgttgtt ttcagggcaa aagacaattg a          951
```

The encoded protein or polypeptide has an amino acid sequence according to SEQ. ID. No. 56 as follows:

```
Val Val Glu Arg Thr Gly Thr Ala Tyr Arg Arg Arg Gly Ala Ala Cys
  1               5                  10                  15

Ser Arg Ile Thr Ser Gln Asn Gln Val Arg Arg Arg Phe Gly Ile Thr
            20                  25                  30

Val Asn Gln Met Gln Lys Thr Ser Leu Leu Ala Leu Ala Phe Ala Ile
        35                  40                  45

Leu Ala Gly Cys Gly Gly Ser Gly Gln Ala Pro Gly Ser Asp Ile Gln
    50                  55                  60

Gly Ala Gln Ala Glu Met Lys Thr Pro Ile Lys Val Asp Leu Asp Ala
 65                  70                  75                  80

Tyr Thr Ser Lys Lys Leu Asp Ala Val Leu Glu Ala Arg Ala Asn Lys
                 85                  90                  95

Ser Tyr Val Asn Lys Gly Gln Leu Ile Asp Leu Val Ser Gly Ala Phe
            100                 105                 110

Leu Gly Thr Pro Tyr Arg Ser Asn Met Leu Val Gly Thr Glu Glu Ile
        115                 120                 125

Pro Glu Gln Leu Val Ile Asp Phe Arg Gly Leu Asp Cys Phe Ala Tyr
    130                 135                 140

Leu Asp Tyr Val Glu Ala Leu Arg Arg Ser Thr Ser Gln Gln Asp Phe
145                 150                 155                 160

Val Arg Asn Leu Val Gln Val Arg Tyr Lys Gly Gly Asp Val Asp Phe
                165                 170                 175

Leu Asn Arg Lys His Phe Phe Thr Asp Trp Ala Tyr Gly Thr Thr His
            180                 185                 190
```

```
Pro Val Ala Asp Asp Ile Thr Thr Gln Ile Ser Pro Gly Ala Val Ser
        195                 200                 205

Val Arg Lys Arg Leu Asn Glu Arg Ala Lys Gly Lys Val Tyr Leu Pro
    210                 215                 220

Gly Leu Pro Val Val Glu Arg Ser Met Thr Tyr Ile Pro Ser Arg Leu
225                 230                 235                 240

Val Asp Ser Gln Val Val Ser His Leu Arg Thr Gly Asp Tyr Ile Gly
                245                 250                 255

Ile Tyr Thr Pro Leu Pro Gly Leu Asp Val Thr His Val Gly Phe Phe
            260                 265                 270

Ile Met Thr Asp Lys Gly Pro Val Leu Arg Asn Ala Ser Ser Arg Lys
        275                 280                 285

Glu Asn Arg Lys Val Met Asp Leu Pro Phe Leu Asp Tyr Val Ser Glu
    290                 295                 300

Lys Pro Gly Ile Val Val Phe Arg Ala Lys Asp Asn
305                 310                 315
```

A DNA molecule from *Pseudomonas syringae* pv. *delphinii* strain PDDCC529 ORF1 encodes a homolog of AvrPphF and has a nucleotide sequence (SEQ. ID. No. 57) as follows:

```
atgaaaaact catttgatct tcttgtcgac ggtttggcga aagactacag catgccgaat 60
ttgccgaaca agaaacacga caatgaagtc tattgcttca cattccagag cgggctcgaa 120
gtaaacattt atcaggacga ctgtcgatgg gtgcatttct ccgccacaat cggacaattt 180
caagacgcca gcaatgacac gctcagccac gcacttcaac tgaacaattt cagtcttgga 240
aagccccttct tcacctttgg aatgaacgga gaaaaggtcg gcgtacttca cacacgcgtt 300
ccgttgattg aaatgaatac cgttgaaatg cgcaaggtat tcgaggactt gctcgatgta 360
gcaggcggca tcagagcgac attcaagctc agttaa                           396
```

The encoded AvrPhpF homolog has an amino acid sequence according to SEQ. ID. No. 58 as follows:

```
Met Lys Asn Ser Phe Asp Leu Leu Val Asp Gly Leu Ala Lys Asp Tyr
  1               5                  10                  15

Ser Met Pro Asn Leu Pro Asn Lys Lys His Asp Asn Glu Val Tyr Cys
             20                  25                  30

Phe Thr Phe Gln Ser Gly Leu Glu Val Asn Ile Tyr Gln Asp Asp Cys
         35                  40                  45

Arg Trp Val His Phe Ser Ala Thr Ile Gly Gln Phe Gln Asp Ala Ser
     50                  55                  60

Asn Asp Thr Leu Ser His Ala Leu Gln Leu Asn Asn Phe Ser Leu Gly
 65                  70                  75                  80

Lys Pro Phe Phe Thr Phe Gly Met Asn Gly Glu Lys Val Gly Val Leu
                 85                  90                  95
```

```
His Thr Arg Val Pro Leu Ile Glu Met Asn Thr Val Glu Met Arg Lys
            100                 105                 110

Val Phe Glu Asp Leu Leu Asp Val Ala Gly Gly Ile Arg Ala Thr Phe
        115                 120                 125

Lys Leu Ser
    130
```

A DNA molecule from *Pseudomonas syringae* pv. *delphinii* strain PDDCC529 ORF1 encodes a homolog of AvrPphF and has a nucleotide sequence (SEQ. ID. No. 59) as follows:

```
atgagtacta tacctggcac ctcgggcgct cacccgattt atagctcaat ttccagccca 60
cgaaatatgt ctggctcgcc cacaccgagt caccgtattg gcggggaaac cctgacctct 120
attcatcagc tctctgccag ccagagagaa caatttctga atactcatga ccccatgaga 180
aaactcagga ttaacaatga tacgccactg tacagaacaa ccgagaagcg ttttatacag 240
gaaggcaaac tggccggcaa tccaaagtct attgcacgtg tcaacttgca cgaagaactg 300
cagcttaatc cgctcgccag tattttaggg aacttacctc acgaggcaag cgcttacttt 360
ccgaaaagcg cccgcgctgc ggatctgaaa gacccttcat tgaatgtaat gacaggctct 420
cgggcaaaaa atgctattcg cggctacgct catgacgacc atgtggcggt caagatgcga 480
ctgggcgact ttcttgaaaa aggcggcaag gtgtacgcgg acacttcatc agtcattgac 540
ggcggagacg aggcgagcgc gctgatcgtt acattgccta aaggacaaaa agttccagtc 600
gagattatcc ctacccataa cgacaacagc aataaaggca gaggctga               648
```

The encoded AvrPphF homolog has an amino acid sequence according to SEQ. ID. No. 60 as follows:

```
Met Ser Thr Ile Pro Gly Thr Ser Gly Ala His Pro Ile Tyr Ser Ser
  1               5                  10                  15

Ile Ser Ser Pro Arg Asn Met Ser Gly Ser Pro Thr Pro Ser His Arg
            20                  25                  30

Ile Gly Gly Glu Thr Leu Thr Ser Ile His Gln Leu Ser Ala Ser Gln
        35                  40                  45

Arg Glu Gln Phe Leu Asn Thr His Asp Pro Met Arg Lys Leu Arg Ile
    50                  55                  60

Asn Asn Asp Thr Pro Leu Tyr Arg Thr Thr Glu Lys Arg Phe Ile Gln
65                  70                  75                  80

Glu Gly Lys Leu Ala Gly Asn Pro Lys Ser Ile Ala Arg Val Asn Leu
                85                  90                  95

His Glu Glu Leu Gln Leu Asn Pro Leu Ala Ser Ile Leu Gly Asn Leu
            100                 105                 110

Pro His Glu Ala Ser Ala Tyr Phe Pro Lys Ser Ala Arg Ala Ala Asp
        115                 120                 125

Leu Lys Asp Pro Ser Leu Asn Val Met Thr Gly Ser Arg Ala Lys Asn
    130                 135                 140

Ala Ile Arg Gly Tyr Ala His Asp Asp His Val Ala Val Lys Met Arg
145                 150                 155                 160
```

```
Leu Gly Asp Phe Leu Glu Lys Gly Gly Lys Val Tyr Ala Asp Thr Ser
                165                 170                 175

Ser Val Ile Asp Gly Gly Asp Glu Ala Ser Ala Leu Ile Val Thr Leu
            180                 185                 190

Pro Lys Gly Gln Lys Val Pro Val Glu Ile Ile Pro Thr His Asn Asp
        195                 200                 205

Asn Ser Asn Lys Gly Arg Gly
    210                 215
```

A DNA molecule from *Pseudomonas syringae* pv. *syringae* strain 226 encodes a homolog of HopPsyA and has a nucleotide sequence (SEQ. ID. No. 61) as follows:

```
gtgaacccta tccatgcacg cttctccagc gtagaagcgc tcagacattc aaacgttgat 60
attcaggcaa tcaaatccga gggtcagttg gaagtcaacg gcaagcgtta cgagattcgt 120
gcggccgctg acggctcaat cgcggtcctc agacccgatc aacagtccaa agcagacaag 180
ttcttcaaag gcgcagcgca tcttattggc ggacaaagcc agcgtgccca aatagcccag 240
gtactcaacg agaaagcggc ggcagttcca cgcctggaca gaatgttggg cagacgcttc 300
gatctggaga agggcggaag tagcgctgtg ggcgccgcaa tcaaggctgc cgacagccga 360
ctgacatcaa aacagacatt tgccagcttc cagcaatggg ctgaaaaagc tgaggcgctc 420
gggcgcgata ccgaaatcgg tatctacatg atctacaaga gggacacgcc agacacaacg 480
cctatgaatg cggcagagca agaacattac ctggaaacgc tacaggctct cgataacaag 540
aaaaacctta tcatacgccc gcagatccat gatgatcggg aagaggaaga gcttgatctg 600
ggccgataca tcgctgaaga cagaaatgcc agaaccggct tttttagaat ggttcctaaa 660
gaccaacgcg cacctgagac aaactcggga cgacttacca ttggtgtaga acctaaatat 720
ggagcgcagt tggccctcgc aatggcaacc ctgatggaca agcacaaatc tgtgacacaa 780
ggtaaagtcg tcggtccggc aaaatatggc cagcaaactg actctgccat tctttacata 840
aatggtgatc ttgcaaaagc agtaaaactg ggcgaaaagc tgaaaaagct gagcggtatc 900
cctcctgaag gattcgtcga acatacaccg ctaagcatgc agtcgacggg tctcggtctt 960
tcttatgccg agtcggttga agggcagcct tccagccacg gacaggcgag aacacacgtt 1020
atcatggatg ccttgaaagg ccagggcccc atggagaaca gactcaaaat ggcgctggca 1080
gaaagaggct atgacccgga aaatccggcg ctcagggcgc gaaactga            1128
```

The encoded HopPsyA homolog has an amino acid sequence according to SEQ. ID. No. 62 as follows:

```
Val Asn Pro Ile His Ala Arg Phe Ser Ser Val Glu Ala Leu Arg His
  1               5                  10                  15

Ser Asn Val Asp Ile Gln Ala Ile Lys Ser Glu Gly Gln Leu Glu Val
             20                  25                  30

Asn Gly Lys Arg Tyr Glu Ile Arg Ala Ala Ala Asp Gly Ser Ile Ala
         35                  40                  45

Val Leu Arg Pro Asp Gln Gln Ser Lys Ala Asp Lys Phe Phe Lys Gly
     50                  55                  60

Ala Ala His Leu Ile Gly Gly Gln Ser Gln Arg Ala Gln Ile Ala Gln
 65                  70                  75                  80

Val Leu Asn Glu Lys Ala Ala Ala Val Pro Arg Leu Asp Arg Met Leu
                 85                  90                  95
```

```
Gly Arg Arg Phe Asp Leu Glu Lys Gly Gly Ser Ser Ala Val Gly Ala
           100                 105                 110

Ala Ile Lys Ala Ala Asp Ser Arg Leu Thr Ser Lys Gln Thr Phe Ala
       115                 120                 125

Ser Phe Gln Gln Trp Ala Glu Lys Ala Glu Ala Leu Gly Arg Asp Thr
   130                 135                 140

Glu Ile Gly Ile Tyr Met Ile Tyr Lys Arg Asp Thr Pro Asp Thr Thr
145                 150                 155                 160

Pro Met Asn Ala Ala Glu Gln Glu His Tyr Leu Glu Thr Leu Gln Ala
               165                 170                 175

Leu Asp Asn Lys Lys Asn Leu Ile Ile Arg Pro Gln Ile His Asp Asp
           180                 185                 190

Arg Glu Glu Glu Glu Leu Asp Leu Gly Arg Tyr Ile Ala Glu Asp Arg
       195                 200                 205

Asn Ala Arg Thr Gly Phe Phe Arg Met Val Pro Lys Asp Gln Arg Ala
   210                 215                 220

Pro Glu Thr Asn Ser Gly Arg Leu Thr Ile Gly Val Glu Pro Lys Tyr
225                 230                 235                 240

Gly Ala Gln Leu Ala Leu Ala Met Ala Thr Leu Met Asp Lys His Lys
               245                 250                 255

Ser Val Thr Gln Gly Lys Val Val Gly Pro Ala Lys Tyr Gly Gln Gln
           260                 265                 270

Thr Asp Ser Ala Ile Leu Tyr Ile Asn Gly Asp Leu Ala Lys Ala Val
       275                 280                 285

Lys Leu Gly Glu Lys Leu Lys Lys Leu Ser Gly Ile Pro Pro Glu Gly
   290                 295                 300

Phe Val Glu His Thr Pro Leu Ser Met Gln Ser Thr Gly Leu Gly Leu
305                 310                 315                 320

Ser Tyr Ala Glu Ser Val Glu Gly Gln Pro Ser Ser His Gly Gln Ala
               325                 330                 335

Arg Thr His Val Ile Met Asp Ala Leu Lys Gly Gln Gly Pro Met Glu
           340                 345                 350

Asn Arg Leu Lys Met Ala Leu Ala Glu Arg Gly Tyr Asp Pro Glu Asn
       355                 360                 365

Pro Ala Leu Arg Ala Arg Asn
   370                 375
```

A DNA molecule from *Pseudomonas syringae* pv. *atrofaciens* strain B143 encodes a homolog of HopPsyA and has a nucleotide sequence (SEQ. ID. No. 63) as follows:

```
atgaacccga tacaaacgcg tttctctaac gtcgaagcac ttagacattc agaggtggat 60
gtacaggagc tcaaagcaca cggtcaaata gaagtgggtg gcaaatgcta cgacattcgc 120
gcggctgcca ataacgacct gactgtccag cgttctgaca aacagatggc gatgagcaag 180
```

```
ttttcaaaa aagcagggtt aagtgggagt tccggcagtc agtccgatca aattgcgcag 240
gtactgaatg acaagcgcgg ctcttccgtt ccccgtctta tacgccaggg gcagacccat 300
ctgggccgta tgcaattcaa catcgaagag gggcaaggca gttcggccgc cacgtccgtc 360
cagaacagca ggctgcccaa tggccgcttg gtaaacagca gtattttgca atgggtcgaa 420
aaggcgaaag ccaatggcag cacaagtacc agtgctcttt atcagatcta cgcaaaagaa 480
ctcccgcgtg tagaactgct gccacgcact gagcaccggg cgtgtctggc gcatatgtat 540
aagctgaacg gtaaggacgg tatcagtatt tggccgcagt ttctggatgg cgtgcgcggg 600
ttgcagctaa aacatgacac aaaagtgttc atgatgaaca accccaaagc agcggacgag 660
ttctacaaga tcgaacgttc gggcacgcaa tttccggatg aggctgtcaa ggcgcgcctg 720
acgataaatg tcaaacctca attccagaag gccatggtcg acgcagcggt caggttgacc 780
gctgagcgtc acgatatcat tactgccaaa gtggcaggtc ctgcaaagat tggcacgatt 840
acagatgcag cggttttcta tgtaagcgga gatttttccg ctgcgcagac acttgcaaaa 900
gagcttcagg cactgctccc tgacgatgcg tttatcaatc atacgccagc tggaatgcaa 960
tccatgggca aggggctgtg ttacgccgag cgtacaccgc aggacaggac aagccacgga 1020
atgtcgcgcg ccagcataat cgagtcggca ctggcagaca ccagcaggtc gtcactggag 1080
aagaagctgc gcaatgcttt caagagcgcc ggatacaatc ccgacaaccc ggcattcagg 1140
ttggaatga                                                        1149
```

The encoded HopPsyA homolog has an amino acid sequence according to SEQ. ID. No. 64 as follows:

```
Met Asn Pro Ile Gln Thr Arg Phe Ser Asn Val Glu Ala Leu Arg His
  1               5                  10                  15

Ser Glu Val Asp Val Gln Glu Leu Lys Ala His Gly Gln Ile Glu Val
             20                  25                  30

Gly Gly Lys Cys Tyr Asp Ile Arg Ala Ala Ala Asn Asn Asp Leu Thr
         35                  40                  45

Val Gln Arg Ser Asp Lys Gln Met Ala Met Ser Lys Phe Phe Lys Lys
     50                  55                  60

Ala Gly Leu Ser Gly Ser Ser Gly Ser Gln Ser Asp Gln Ile Ala Gln
 65                  70                  75                  80

Val Leu Asn Asp Lys Arg Gly Ser Ser Val Pro Arg Leu Ile Arg Gln
                 85                  90                  95

Gly Gln Thr His Leu Gly Arg Met Gln Phe Asn Ile Glu Glu Gly Gln
            100                 105                 110

Gly Ser Ser Ala Ala Thr Ser Val Gln Asn Ser Arg Leu Pro Asn Gly
        115                 120                 125

Arg Leu Val Asn Ser Ser Ile Leu Gln Trp Val Glu Lys Ala Lys Ala
    130                 135                 140

Asn Gly Ser Thr Ser Thr Ser Ala Leu Tyr Gln Ile Tyr Ala Lys Glu
145                 150                 155                 160

Leu Pro Arg Val Glu Leu Leu Pro Arg Thr Glu His Arg Ala Cys Leu
                165                 170                 175

Ala His Met Tyr Lys Leu Asn Gly Lys Asp Gly Ile Ser Ile Trp Pro
            180                 185                 190

Gln Phe Leu Asp Gly Val Arg Gly Leu Gln Leu Lys His Asp Thr Lys
        195                 200                 205

Val Phe Met Met Asn Asn Pro Lys Ala Ala Asp Glu Phe Tyr Lys Ile
    210                 215                 220
```

```
Glu Arg Ser Gly Thr Gln Phe Pro Asp Glu Ala Val Lys Ala Arg Leu
225                 230                 235                 240

Thr Ile Asn Val Lys Pro Gln Phe Gln Lys Ala Met Val Asp Ala Ala
                245                 250                 255

Val Arg Leu Thr Ala Glu Arg His Asp Ile Ile Thr Ala Lys Val Ala
            260                 265                 270

Gly Pro Ala Lys Ile Gly Thr Ile Thr Asp Ala Ala Val Phe Tyr Val
        275                 280                 285

Ser Gly Asp Phe Ser Ala Ala Gln Thr Leu Ala Lys Glu Leu Gln Ala
    290                 295                 300

Leu Leu Pro Asp Asp Ala Phe Ile Asn His Thr Pro Ala Gly Met Gln
305                 310                 315                 320

Ser Met Gly Lys Gly Leu Cys Tyr Ala Glu Arg Thr Pro Gln Asp Arg
                325                 330                 335

Thr Ser His Gly Met Ser Arg Ala Ser Ile Ile Glu Ser Ala Leu Ala
            340                 345                 350

Asp Thr Ser Arg Ser Ser Leu Glu Lys Lys Leu Arg Asn Ala Phe Lys
        355                 360                 365

Ser Ala Gly Tyr Asn Pro Asp Asn Pro Ala Phe Arg Leu Glu
    370                 375                 380
```

A DNA molecule from *Pseudomonas syringae* pv. *tomato* strain DC3000 encodes a homolog of HopPtoA, identified herein as HopPtoA2, and has a nucleotide sequence (SEQ. ID. No. 65) as follows:

```
atgcacatca accaatccgc ccaacaaccg cctggcgttg caatggagag ttttcggaca 60
gcttccgacg cgtcccttgc ttcgagttct gtgcggtctg tcagcactac ctcgtgccgc 120
gatctacaag ctattaccga ttatctgaaa catcacgtgt tcgctgcgca caggttttcg 180
gtaataggct caccggatga gcgtgatgcc gctcttgcac acaacgagca gatcgatgcg 240
ttggtagaga cacgcgccaa ccgcctgtac tccgaagggg agacccccgc aaccatcgcc 300
gaaacattcg ccaaggcgga aaagttcgac cgtttggcga cgaccgcatc aagtgctttt 360
gagaacacgc catttgccgc tgcctcggtg cttcagtaca tgcagcctgc gatcaacaag 420
ggcgattggc tagcaacgcc gctcaagccg ctgaccccgc tcatttccgg agcgctgtcg 480
ggagccatgg accaggtggg caccaaaatg atggatcgtg cgaggggtga tctgcattac 540
ctgagcactt cgccggacaa gttgcatgat gcgatggccg tatcggtgaa gcgccactcg 600
cctgcgcttg gtcgacaggt tgtggacatg gggattgcag tgcagacgtt ctcggcgcta 660
aatgtggtgc gtaccgtatt ggctccagca ctagcgtcca gaccgtcggt gcagggtgct 720
gttgattttg gcgtatctac ggcgggtggc ttggttgcga atgcaggctt tggcgaccgc 780
atgctcagtg tgcaatcgcg cgatcaactg cgtgggggggg cattcgtact tggcatgaaa 840
gataaagagc ccaaggccgc gttgagtgaa gaaactgatt ggcttgatgc ttacaaagcg 900
atcaagtcgg ccagctactc aggtgcggcg ctcaatgcgg gcaagcggat ggccggcctg 960
ccactggacg tcgcgaccga cgggctcaag gcggtgagaa gtctggtgtc ggccaccagc 1020
ctgacaaaaa atggcctggc cctagccggt ggttacgccg gggtaagtaa gttgcagaaa 1080
atggcgacga aaaatatcac tgattcggcg accaaggctg cggttagtca gctgagcaac 1140
ctggtgggtt cggtaggcgt ttcgcaggc tggaccaccg ctggactggc gactgaccct 1200
gcggttaaga aagccgagtc gtttatacag gataaggtga aatcgaccgc atctagtacc 1260
acaagctatg ttgccgacca gaccgtcaaa ctggcgaaaa cagtcaagga catgagcggg 1320
gaggcgatct ccagcaccgg tgccagctta cgcagtactg tcaataacct gcgtcatcgc 1380
tccgctccgg aagctgatat cgaagaaggt gggatttcgg cgttttctcg aagtgaaaca 1440
ccgtttcagc tcaggcgttt gtaa                                       1464
```

Although *hopPtoA2* does not lie within the CEL, it is included here as a homolog of *hopPtoA*, which corresponds to CEL *ORF5* as noted above. The encoded HopPtoA2 protein or polypeptide has an amino acid sequence according to SEQ. ID. No. 66 as follows:

```
Met His Ile Asn Gln Ser Ala Gln Gln Pro Pro Gly Val Ala Met Glu
 1               5                  10                  15

Ser Phe Arg Thr Ala Ser Asp Ala Ser Leu Ala Ser Ser Ser Val Arg
            20                  25                  30

Ser Val Ser Thr Thr Ser Cys Arg Asp Leu Gln Ala Ile Thr Asp Tyr
        35                  40                  45

Leu Lys His His Val Phe Ala Ala His Arg Phe Ser Val Ile Gly Ser
    50                  55                  60

Pro Asp Glu Arg Asp Ala Ala Leu Ala His Asn Glu Gln Ile Asp Ala
65                  70                  75                  80

Leu Val Glu Thr Arg Ala Asn Arg Leu Tyr Ser Glu Gly Glu Thr Pro
                85                  90                  95

Ala Thr Ile Ala Glu Thr Phe Ala Lys Ala Glu Lys Phe Asp Arg Leu
            100                 105                 110

Ala Thr Thr Ala Ser Ser Ala Phe Glu Asn Thr Pro Phe Ala Ala Ala
        115                 120                 125

Ser Val Leu Gln Tyr Met Gln Pro Ala Ile Asn Lys Gly Asp Trp Leu
    130                 135                 140

Ala Thr Pro Leu Lys Pro Leu Thr Pro Leu Ile Ser Gly Ala Leu Ser
145                 150                 155                 160

Gly Ala Met Asp Gln Val Gly Thr Lys Met Met Asp Arg Ala Arg Gly
                165                 170                 175

Asp Leu His Tyr Leu Ser Thr Ser Pro Asp Lys Leu His Asp Ala Met
            180                 185                 190

Ala Val Ser Val Lys Arg His Ser Pro Ala Leu Gly Arg Gln Val Val
        195                 200                 205

Asp Met Gly Ile Ala Val Gln Thr Phe Ser Ala Leu Asn Val Val Arg
    210                 215                 220

Thr Val Leu Ala Pro Ala Leu Ala Ser Arg Pro Ser Val Gln Gly Ala
225                 230                 235                 240

Val Asp Phe Gly Val Ser Thr Ala Gly Gly Leu Val Ala Asn Ala Gly
                245                 250                 255

Phe Gly Asp Arg Met Leu Ser Val Gln Ser Arg Asp Gln Leu Arg Gly
            260                 265                 270

Gly Ala Phe Val Leu Gly Met Lys Asp Lys Glu Pro Lys Ala Ala Leu
        275                 280                 285

Ser Glu Glu Thr Asp Trp Leu Asp Ala Tyr Lys Ala Ile Lys Ser Ala
    290                 295                 300
```

```
Ser Tyr Ser Gly Ala Ala Leu Asn Ala Gly Lys Arg Met Ala Gly Leu
305                 310                 315                 320

Pro Leu Asp Val Ala Thr Asp Gly Leu Lys Ala Val Arg Ser Leu Val
                325                 330                 335

Ser Ala Thr Ser Leu Thr Lys Asn Gly Leu Ala Leu Ala Gly Gly Tyr
            340                 345                 350

Ala Gly Val Ser Lys Leu Gln Lys Met Ala Thr Lys Asn Ile Thr Asp
        355                 360                 365

Ser Ala Thr Lys Ala Ala Val Ser Gln Leu Ser Asn Leu Val Gly Ser
    370                 375                 380

Val Gly Val Phe Ala Gly Trp Thr Thr Ala Gly Leu Ala Thr Asp Pro
385                 390                 395                 400

Ala Val Lys Lys Ala Glu Ser Phe Ile Gln Asp Lys Val Lys Ser Thr
                405                 410                 415

Ala Ser Ser Thr Thr Ser Tyr Val Ala Asp Gln Thr Val Lys Leu Ala
            420                 425                 430

Lys Thr Val Lys Asp Met Ser Gly Glu Ala Ile Ser Ser Thr Gly Ala
        435                 440                 445

Ser Leu Arg Ser Thr Val Asn Asn Leu Arg His Arg Ser Ala Pro Glu
    450                 455                 460

Ala Asp Ile Glu Glu Gly Gly Ile Ser Ala Phe Ser Arg Ser Glu Thr
465                 470                 475                 480

Pro Phe Gln Leu Arg Arg Leu
                485
```

Fragments of the above-identified proteins or polypeptides as well as fragments of full length proteins from the EELs and CELs of other bacteria, in particular Gram-negative pathogens, can also be used according to the present invention.

Suitable fragments can be produced by several means. Subclones of the gene encoding a known protein can be produced using conventional molecular genetic manipulation for subcloning gene fragments, such as described by Sambrook et al., 1989, and Ausubel et al., 1994. The subclones then are expressed *in vitro* or *in vivo* in bacterial cells to yield a smaller protein or polypeptide that can be tested for activity, e.g., as a product required for pathogen virulence.

In another approach, based on knowledge of the primary structure of the protein, fragments of the protein-coding gene may be synthesized using the PCR technique together with specific sets of primers chosen to represent particular portions of the protein (Erlich et al., 1991). These can then be cloned into an appropriate

vector for expression of a truncated protein or polypeptide from bacterial cells as described above.

As an alternative, fragments of a protein can be produced by digestion of a full-length protein with proteolytic enzymes like chymotrypsin or *Staphylococcus* proteinase A, or trypsin. Different proteolytic enzymes are likely to cleave different proteins at different sites based on the amino acid sequence of the particular protein. Some of the fragments that result from proteolysis may be active virulence proteins or polypeptides.

Chemical synthesis can also be used to make suitable fragments. Such a synthesis is carried out using known amino acid sequences for the polyppetide being produced. Alternatively, subjecting a full length protein to high temperatures and pressures will produce fragments. These fragments can then be separated by conventional procedures (e.g., chromatography, SDS-PAGE).

Variants may also (or alternatively) be modified by, for example, the deletion or addition of amino acids that bave minimal influence on the properties, secondary structure and hydropathic nature of the polypeptide. For example, a polypeptide may be conjugated to a signal (or leader) sequence at the N-terminal end of the protein which co-translationally or post-translationally directs transfer of the protein. The polypeptide may also be conjugated to a linker or other sequence for ease of synthesis, purification, or identification of the polypeptide.

The proteins or polypeptides used in accordance with the present invention are preferably produced in purified form (preferably at least about 80%, more preferably 90%, pure) by conventional techniques. Typically, the protein or polypeptide of the present invention is secreted into the growth medium of recombinant host cells (discussed *infra*). Alternatively, the protein or polypeptide of the present invention is produced but not secreted into growth medium. In such cases, to isolate the protein, the host cell (e.g., *E. coli*) carrying a recombinant plasmid is propagated, lysed by sonication, heat, or chemical treatment, and the homogenate is centrifuged to remove bacterial debris. The supernatant is then subjected to sequential ammonium sulfate precipitation. The fraction containing the protein or polypeptide of interest is subjected to gel filtration in an appropriately sized dextran

or polyacrylamide column to separate the proteins. If necessary, the protein fraction may be further purified by HPLC.

DNA molecules encoding other EEL and CEL protein or polypeptides can be identified using a PCR-based methodology for cloning portions of the pathogenicity islands of a bacterium. Basically, the PCR-based strategy involves the use of conserved sequences from the *hrpK* and *tRNA*^{leu} genes (or other conserved border sequences) as primers for cloning EEL intervening regions of the pathogenicity island. As shown in Figures 2B-C, the *hrpK* and *tRNA*^{leu} genes are highly conserved among diverse *Pseudomonas syringae* variants. Depending upon the size of EEL, additional primers can be prepared from the originally obtained cDNA sequence, allowing for recovery of clones and walking through the EEL in a step-wise fashion. If full-length coding sequences are not obtained from the PCR steps, contigs can be assembled to prepare full-length coding sequences using suitable restriction enzymes. Similar PCR-based procedures can be used for obtaining clones that encode open reading frames in the CEL. As shown in Figure 3, the CEL of diverse *Pseudomonas syringae* pathovars contain numerous conserved domains. Moreover, known sequences of the *hrp/hrc* domain, *hrpW*, *AvrE*, or *gstA* can be used to prepare primers.

Using the above-described PCR-based methods, a number of DNA sequences were utilized as the source for primers. One such DNA molecule is isolated from the *tRNA*^{leu} gene of *Pseudomonas syringae* pv. tomato DC3000, which has a nucleotide sequence (SEQ. ID. No. 67) as follows:

```
gccctgatgg cggaattggt agacgcggcg gattcaaaat ccgttttcga aagaagtggg      60
agttcgattc tccctcgggg caccacca                                        88
```

An additional DNA molecule which can be used to supply suitable primers is from the *tRNA*^{leu} gene of *Pseudomonas syringae* pv. *syringae* B728a, which has a nucleotide sequence (SEQ. ID. No. 68) as follows:

```
gccctgatgg cggaattggt agacgcggcg gattcaaaat ccgttttcga aagaagtggg      60
agttcgattc tccctcgggg cacca                                           85
```

Another DNA molecule is isolated from the *queA* gene of *Pseudomonas syringae* pv. tomato DC3000, which has a nucleotide sequence (SEQ. ID. No. 69) as follows:

```
atgcgcgtcg ctgactttac cttcgaactc cccgattccc tgattgctcg tcacccgttg 60
gccgagcgtc gcagcagtcg tctgttgacc cttgatgggc cgacgggcgc gctggcacat 120
cgtcaattca ccgatttgct cgagcatttg cgctcgggcg acttgatggt gttcaacaat 180
acccgtgtca ttcccgcacg tttgttcggg cagaaggcgt ccggcggcaa gctggagatt 240
ctggtcgagc gcgtgctgga cagccatcgt gtgctggcgc acgtgcgtgc cagcaagtcg 300
ccaaagccgg gctcgtcgat cctgatcgat ggcggcggcg aggccgagat ggtggcgcgg 360
catgacgcgc tgttcgagtt gcgctttgcc gaagaagtgc tgccgttgct ggatcgtgtc 420
ggccatatgc cgttgcctcc ttatatagac cgcccggacg aaggtgccga ccgcgagcgt 480
tatcagaccg tttacgccca gcgcgccggt gctgtggcgg cgccgactgc cggcctgcat 540
ttcgaccagc cgttgatgga agcaattgcc gccaagggcg tcgagactgc ttttgtcact 600
ctgcacgtcg gcgcgggtac gttccagccg gtgcgtgtcg agcagatcga agatcaccac 660
atgcacagcg aatggctgga agtcagccag gacgtggtcg atgccgtggc ggcgtgccgt 720
gcgcggggcg ggcgggtgat tgcggtcggg accaccagcg tgcgttcgct ggagagtgcc 780
gcgcgtgatg gccagttgaa gccgtttagc ggcgacaccg acatcttcat ctatccgggg 840
cggccgtttc atgtggtcga tgccctggtg actaattttc atttgcctga atccacgctg 900
ttgatgctgg tttcggcgtt cgccggttat cccgaaacca tggcggccta cgcggcggcc 960
atcgaacacg ggtaccgctt cttcagttac ggtgatgcca tgttcatcac ccgcaatccc 1020
gcgccgacgg ccccacagga atcggcacca gaggatcacg catga                  1065
```

This DNA molecule encodes QueA, which has an amino acid sequence (SEQ. ID. No. 70) as follows:

```
Met Arg Val Ala Asp Phe Thr Phe Glu Leu Pro Asp Ser Leu Ile Ala
  1               5                  10                  15

Arg His Pro Leu Ala Glu Arg Arg Ser Ser Arg Leu Leu Thr Leu Asp
            20                  25                  30

Gly Pro Thr Gly Ala Leu Ala His Arg Gln Phe Thr Asp Leu Leu Glu
        35                  40                  45

His Leu Arg Ser Gly Asp Leu Met Val Phe Asn Asn Thr Arg Val Ile
    50                  55                  60

Pro Ala Arg Leu Phe Gly Gln Lys Ala Ser Gly Gly Lys Leu Glu Ile
65                  70                  75                  80

Leu Val Glu Arg Val Leu Asp Ser His Arg Val Leu Ala His Val Arg
                85                  90                  95

Ala Ser Lys Ser Pro Lys Pro Gly Ser Ser Ile Leu Ile Asp Gly Gly
            100                 105                 110

Gly Glu Ala Glu Met Val Ala Arg His Asp Ala Leu Phe Glu Leu Arg
        115                 120                 125

Phe Ala Glu Glu Val Leu Pro Leu Leu Asp Arg Val Gly His Met Pro
    130                 135                 140

Leu Pro Pro Tyr Ile Asp Arg Pro Asp Glu Gly Ala Asp Arg Glu Arg
145                 150                 155                 160

Tyr Gln Thr Val Tyr Ala Gln Arg Ala Gly Ala Val Ala Ala Pro Thr
                165                 170                 175

Ala Gly Leu His Phe Asp Gln Pro Leu Met Glu Ala Ile Ala Ala Lys
            180                 185                 190

Gly Val Glu Thr Ala Phe Val Thr Leu His Val Gly Ala Gly Thr Phe
        195                 200                 205
```

```
Gln Pro Val Arg Val Glu Gln Ile Glu Asp His His Met His Ser Glu
    210                 215                 220

Trp Leu Glu Val Ser Gln Asp Val Val Asp Ala Val Ala Ala Cys Arg
225                 230                 235                 240

Ala Arg Gly Gly Arg Val Ile Ala Val Gly Thr Thr Ser Val Arg Ser
                245                 250                 255

Leu Glu Ser Ala Ala Arg Asp Gly Gln Leu Lys Pro Phe Ser Gly Asp
            260                 265                 270

Thr Asp Ile Phe Ile Tyr Pro Gly Arg Pro Phe His Val Val Asp Ala
        275                 280                 285

Leu Val Thr Asn Phe His Leu Pro Glu Ser Thr Leu Leu Met Leu Val
    290                 295                 300

Ser Ala Phe Ala Gly Tyr Pro Glu Thr Met Ala Ala Tyr Ala Ala Ala
305                 310                 315                 320

Ile Glu His Gly Tyr Arg Phe Phe Ser Tyr Gly Asp Ala Met Phe Ile
                325                 330                 335

Thr Arg Asn Pro Ala Pro Thr Ala Pro Gln Glu Ser Ala Pro Glu Asp
            340                 345                 350

His Ala
```

DNA molecules encoding other EEL and CEL proteins or polypeptides can also be identified by determining whether such DNA molecules hybridize under stringent conditions to a DNA molecule as identified above. An example of suitable stringency conditions is when hybridization is carried out at a temperature of about 37°C using a hybridization medium that includes 0.9M sodium citrate ("SSC") buffer, followed by washing with 0.2x SSC buffer at 37°C. Higher stringency can readily be attained by increasing the temperature for either hybridization or washing conditions or increasing the sodium concentration of the hybridization or wash medium. Nonspecific binding may also be controlled using any one of a number of known techniques such as, for example, blocking the membrane with protein-containing solutions, addition of heterologous RNA, DNA, and SDS to the hybridization buffer, and treatment with RNase. Wash conditions are typically performed at or below stringency. Exemplary high stringency conditions include carrying out hybridization at a temperature of about 42°C to about 65°C for up to about 20 hours in a hybridization medium containing 1M NaCl, 50 mM Tris-HCl, pH 7.4, 10 mM EDTA, 0.1% sodium dodecyl sulfate (SDS), 0.2% ficoll, 0.2% polyvinylpyrrolidone, 0.2%

bovine serum albumin, and 50 μg/ml *E. coli* DNA, followed by washing carried out at between about 42°C to about 65°C in a 0.2x SSC buffer.

Also encompassed by the present invention are nucleic acid molecules which contain conserved substitutions as compared to the above identified DNA molecules and, thus, encode the same protein or polypeptides identified above. Further, complementary sequences are also encompassed by the present invention.

The nucleic acid of the present invention can be either DNA or RNA, which can readily be prepared using the above identified DNA molecules of the present invention.

The delivery of effector proteins or polypeptides can be achieved in several ways, depending upon the host being treated and the materials being used: (1) as a stable or plasmid-encoded transgene; (2) transiently expressed via *Agrobacterium* or viral vectors; (3) delivered by the type III secretion systems of disarmed pathogens or recombinant nonpathogenic bacteria which express a functional, heterologous type III secretion system; or (4) delivered via topical application followed by TAT protein transduction domain-mediated spontaneous uptake into cells. Each of these is discussed *infra*.

The DNA molecule encoding the protein or polypeptide can be incorporated in cells using conventional recombinant DNA technology. Generally, this involves inserting the DNA molecule into an expression system to which the DNA molecule is heterologous (i.e. not normally present). The heterologous DNA molecule is inserted into the expression system or vector in proper sense orientation and correct reading frame. The vector contains the necessary elements for the transcription and translation of the inserted protein-coding sequences.

U.S. Patent No. 4,237,224 to Cohen and Boyer describes the production of expression systems in the form of recombinant plasmids using restriction enzyme cleavage and ligation with DNA ligase. These recombinant plasmids are then introduced by means of transformation and replicated in unicellular cultures including prokaryotic organisms and eukaryotic cells grown in tissue culture.

Recombinant genes may also be introduced into viruses, such as vaccina virus. Recombinant viruses can be generated by transfection of plasmids into cells infected with virus.

Suitable vectors include, but are not limited to, the following viral vectors such as lambda vector system gt11, gt WES.tB, Charon 4, and plasmid vectors such as pBR322, pBR325, pACYC177, pACYC1084, pUC8, pUC9, pUC18, pUC19, pLG339, pR290, pKC37, pKC101, SV 40, pBluescript II SK +/- or KS +/- (see "Stratagene Cloning Systems" Catalog (1993) from Stratagene, La Jolla, Calif, which is hereby incorporated by reference), pQE, pIH821, pGEX, pET series (see Studier et al., 1990). Recombinant molecules can be introduced into cells via transformation, particularly transduction, conjugation, mobilization, or electroporation. The DNA sequences are cloned into the vector using standard cloning procedures in the art, as described by Sambrook et al., 1989.

A variety of host-vector systems may be utilized to express the protein-encoding sequence(s). Primarily, the vector system must be compatible with the host cell used. Host-vector systems include, but are not limited to, the following: bacteria transformed with bacteriophage DNA, plasmid DNA, or cosmid DNA; microorganisms such as yeast containing yeast vectors; mammalian cell systems infected with virus (e.g., vaccinia virus, adenovirus, etc.); insect cell systems infected with virus (e.g., baculovirus); and plant cells infected by bacteria. The expression elements of these vectors vary in their strength and specificities. Depending upon the host-vector system utilized, any one of a number of suitable transcription and translation elements can be used.

Different genetic signals and processing events control many levels of gene expression (e.g., DNA transcription and messenger RNA (mRNA) translation).

Transcription of DNA is dependent upon the presence of a promoter which is a DNA sequence that directs the binding of RNA polymerase and thereby promotes mRNA synthesis. The DNA sequences of eukaryotic promoters differ from those of prokaryotic promoters. Eukaryotic promoters and accompanying genetic signals may not be recognized in or may not function in a prokaryotic system and, further, prokaryotic promoters are not recognized and do not function in eukaryotic cells.

Similarly, translation of mRNA in prokaryotes depends upon the presence of the proper prokaryotic signals which differ from those of eukaryotes. Efficient translation of mRNA in prokaryotes requires a ribosome binding site called

the Shine-Dalgarno ("SD") sequence on the mRNA. This sequence is a short nucleotide sequence of mRNA that is located before the start codon, usually AUG, which encodes the amino-terminal methionine of the protein. The SD sequences are complementary to the 3'-end of the 16S rRNA (ribosomal RNA) and probably promote binding of mRNA to ribosomes by duplexing with the rRNA to allow correct positioning of the ribosome. For a review on maximizing gene expression, see Roberts and Lauer, 1979.

Promoters vary in their "strength" (i.e., their ability to promote transcription). For the purposes of expressing a cloned gene, it is desirable to use strong promoters in order to obtain a high level of transcription and, hence, expression of the gene. Depending upon the host cell system utilized, any one of a number of suitable promoters may be used. For instance, when cloning in *E. coli*, its bacteriophages, or plasmids, promoters such as the T7 phage promoter, *lac* promoter, *trp* promoter, *rec*A promoter, ribosomal RNA promoter, the P_R and P_L promoters of coliphage lambda and others, including but not limited, to *lac*UV5, *omp*F, *bla*, *lpp*, and the like, may be used to direct high levels of transcription of adjacent DNA segments. Additionally, a hybrid *trp-lac*UV5 (*tac*) promoter or other *E. coli* promoters produced by recombinant DNA or other synthetic DNA techniques may be used to provide for transcription of the inserted gene.

Bacterial host cell strains and expression vectors may be chosen which inhibit the action of the promoter unless specifically induced. In certain operations, the addition of specific inducers is necessary for efficient transcription of the inserted DNA. For example, the *lac* operon is induced by the addition of lactose or IPTG (isopropylthio-beta-D-galactoside). A variety of other operons, such as *trp*, *pro*, etc., are under different controls.

Specific initiation signals are also required for efficient gene transcription and translation in prokaryotic cells. These transcription and translation initiation signals may vary in "strength" as measured by the quantity of gene specific messenger RNA and protein synthesized, respectively. The DNA expression vector, which contains a promoter, may also contain any combination of various "strong" transcription and/or translation initiation signals. For instance, efficient translation in *E. coli* requires an SD sequence about 7-9 bases 5' to the initiation codon ("ATG") to

provide a ribosome binding site. Thus, any SD-ATG combination that can be utilized by host cell ribosomes may be employed. Such combinations include but are not limited to the SD-ATG combination from the *cro* gene or the *N* gene of coliphage lambda, or from the *E. coli* tryptophan E, D, C, B or A genes. Additionally, any SD-ATG combination produced by recombinant DNA or other techniques involving incorporation of synthetic nucleotides may be used.

Once the isolated DNA molecule encoding the polypeptide or protein has been cloned into an expression system, it is ready to be incorporated into a host cell. Such incorporation can be carried out by the various forms of transformation noted above, depending upon the vector/host cell system. Suitable host cells include, but are not limited to, bacteria, virus, yeast, mammalian cells, insect, plant, and the like.

Because it is desirable for recombinant host cells to secrete the encoded protein or polypeptide, it is preferable that the host cell also possess a functional type III secretion system. The type III secretion system can be heterologous to host cell (Ham et al., 1998) or the host cell can naturally possess a type III secretion system. Host cells which naturally contain a type III secretion system include many pathogenic Gram-negative bacterium, such as numerous *Erwinia* species, *Pseudomonas* species, *Xanthomonas* species, etc. Other type III secretion systems are known and still others are continually being identified. Pathogenic bacteria that can be utilized to deliver effector proteins or polypeptides are preferably disarmed according to known techniques, i.e., as described above. Alternatively, isolation of the effector protein or polypeptide from the host cell or growth medium can be carried out as described above.

Another aspect of the present invention relates to a transgenic plant which express a protein or polypeptide of the present invention and methods of making the same.

In order to express the DNA molecule in isolated plant cells or tissue or whole plants, a plant expressible promoter is needed. Any plant-expressible promoter can be utilized regardless of its origin, i.e., viral, bacterial, plant, etc. Without limitation, two suitable promoters include the nopaline synthase promoter (Fraley et al., 1983) and the cauliflower mosaic virus 35S promoter (O'Dell et al.,

1985). Both of these promoters yield constitutive expression of coding sequences under their regulatory control.

While constitutive expression is generally suitable for expression of the DNA molecule, it should be apparent to those of skill in the art that temporally or tissue regulated expression may also be desirable, in which case any regulated promoter can be selected to achieve the desired expression. Typically, the temporally or tissue regulated promoters will be used in connection with the DNA molecule that are expressed at only certain stages of development or only in certain tissues.

In some plants, it may also be desirable to use promoters which are responsive to pathogen infiltration or stress. For example, it may be desirable to limit expression of the protein or polypeptide in response to infection by a particular pathogen of the plant. One example of a pathogen-inducible promoter is the *gst1* promoter from potato, which is described in U.S. Patent Nos. 5,750,874 and 5,723,760 to Strittmayer et al., which are hereby incorporated by reference.

Expression of the DNA molecule in isolated plant cells or tissue or whole plants also requires appropriate transcription termination and polyadenylation of mRNA. Any 3' regulatory region suitable for use in plant cells or tissue can be operably linked to the first and second DNA molecules. A number of 3' regulatory regions are known to be operable in plants. Exemplary 3' regulatory regions include, without limitation, the nopaline synthase 3' regulatory region (Fraley et al., 1983) and the cauliflower mosaic virus 3' regulatory region (Odell et al., 1985).

The promoter and a 3' regulatory region can readily be ligated to the DNA molecule using well known molecular cloning techniques described in Sambrook et al., 1989.

One approach to transforming plant cells with a DNA molecule of the present invention is particle bombardment (also known as biolistic transformation) of the host cell. This can be accomplished in one of several ways. The first involves propelling inert or biologically active particles at cells. This technique is disclosed in U.S. Patent Nos. 4,945,050, 5,036,006, and 5,100,792, all to Sanford, et al. Generally, this procedure involves propelling inert or biologically active particles at the cells under conditions effective to penetrate the outer surface of the cell and to be incorporated within the interior thereof. When inert particles are utilized, the vector

can be introduced into the cell by coating the particles with the vector containing the heterologous DNA. Alternatively, the target cell can be surrounded by the vector so that the vector is carried into the cell by the wake of the particle. Biologically active particles (e.g., dried bacterial cells containing the vector and heterologous DNA) can also be propelled into plant cells. Other variations of particle bombardment, now known or hereafter developed, can also be used.

Another method of introducing the DNA molecule into plant cells is fusion of protoplasts with other entities, either minicells, cells, lysosomes, or other fusible lipid-surfaced bodies that contain the DNA molecule (Fraley et al., 1982).

The DNA molecule may also be introduced into the plant cells by electroporation (Fromm, et al., 1985). In this technique, plant protoplasts are electroporated in the presence of plasmids containing the DNA molecule. Electrical impulses of high field strength reversibly permeabilize biomembranes allowing the introduction of the plasmids. Electroporated plant protoplasts reform the cell wall, divide, and regenerate.

Another method of introducing the DNA molecule into plant cells is to infect a plant cell with *Agrobacterium tumefaciens* or *Agrobacterium rhizogenes* previously transformed with the DNA molecule. Under appropriate conditions known in the art, the transformed plant cells are grown to form shoots or roots, and develop further into plants. Generally, this procedure involves inoculating the plant tissue with a suspension of bacteria and incubating the tissue for 48 to 72 hours on regeneration medium without antibiotics at 25-28°C.

Agrobacterium is a representative genus of the Gram-negative family Rhizobiaceae. Its species are responsible for crown gall (*A. tumefaciens*) and hairy root disease (*A. rhizogenes*). The plant cells in crown gall tumors and hairy roots are induced to produce amino acid derivatives known as opines, which are catabolized only by the bacteria. The bacterial genes responsible for expression of opines are a convenient source of control elements for chimeric expression cassettes. In addition, assaying for the presence of opines can be used to identify transformed tissue.

Heterologous genetic sequences such as a DNA molecule of the present invention can be introduced into appropriate plant cells by means of the Ti plasmid of *A. tumefaciens* or the Ri plasmid of *A. rhizogenes*. The Ti or Ri plasmid

is transmitted to plant cells on infection by *Agrobacterium* and is stably integrated into the plant genome (Schell, 1987).

Plant tissue suitable for transformation include leaf tissue, root tissue, meristems, zygotic and somatic embryos, and anthers.

After transformation, the transformed plant cells can be selected and regenerated.

Preferably, transformed cells are first identified using, e.g., a selection marker simultaneously introduced into the host cells along with the DNA molecule of the present invention. Suitable selection markers include, without limitation, markers coding for antibiotic resistance, such as kanamycin resistance (Fraley et al., 1983). A number of antibiotic-resistance markers are known in the art and other are continually being identified. Any known antibiotic-resistance marker can be used to transform and select transformed host cells in accordance with the present invention. Cells or tissues are grown on a selection media containing an antibiotic, whereby generally only those transformants expressing the antibiotic resistance marker continue to grow.

Once a recombinant plant cell or tissue has been obtained, it is possible to regenerate a full-grown plant therefrom. Thus, another aspect of the present invention relates to a transgenic plant that includes a DNA molecule of the present invention, wherein the promoter induces transcription of the first DNA molecule in response to infection of the plant by an oomycete. Preferably, the DNA molecule is stably inserted into the genome of the transgenic plant of the present invention.

Plant regeneration from cultured protoplasts is described in Evans et al., 1983, and Vasil, 1984 and 1986.

It is known that practically all plants can be regenerated from cultured cells or tissues, including but not limited to, all major species of rice, wheat, barley, rye, cotton, sunflower, peanut, corn, potato, sweet potato, bean, pea, chicory, lettuce, endive, cabbage, cauliflower, broccoli, turnip, radish, spinach, onion, garlic, eggplant, pepper, celery, carrot, squash, pumpkin, zucchini, cucumber, apple, pear, melon, strawberry, grape, raspberry, pineapple, soybean, tobacco, tomato, sorghum, and sugarcane.

Means for regeneration vary from species to species of plants, but generally a suspension of transformed protoplasts or a petri plate containing

transformed explants is first provided. Callus tissue is formed and shoots may be induced from callus and subsequently rooted. Alternatively, embryo formation can be induced in the callus tissue. These embryos germinate as natural embryos to form plants. The culture media will generally contain various amino acids and hormones, such as auxin and cytokinins. It is also advantageous to add glutamic acid and proline to the medium, especially for such species as corn and alfalfa. Efficient regeneration will depend on the medium, on the genotype, and on the history of the culture. If these three variables are controlled, then regeneration is usually reproducible and repeatable.

After the DNA molecule is stably incorporated in transgenic plants, it can be transferred to other plants by sexual crossing or by preparing cultivars. With respect to sexual crossing, any of a number of standard breeding techniques can be used depending upon the species to be crossed. Cultivars can be propagated in accord with common agricultural procedures known to those in the field.

Diseases caused by the vast majority of bacterial pathogens result in limited lesions. That is, even when everything is working in the pathogen's favor (e.g., no triggering of the hypersensitive response because of *R*-gene detection of one of the effectors), the parasitic process still triggers defenses after a couple of days, which then stops the infection from spreading. Thus, the very same effectors that enable parasitism to proceed must also eventually trigger defenses. Therefore, premature expression of these effectors is believed to "turn on" plant defenses earlier (i.e., prior to infection) and make the plant resistant to either the specific bacteria from which the effector protein was obtained or many pathogens. An advantage of this approach is that it involves natural products and plants seem highly sensitive to pathogen effector proteins.

According to one embodiment, a transgenic plant is provided that contains a heterologous DNA molecule of the present invention. Preferably, the heterologous DNA molecule is derived from a plant pathogen EEL. When the heterologous DNA molecule is expressed in the transgenic plant, plant defenses are activated, imparting disease resistance to the transgenic plant. The transgenic plant can also contain an *R*-gene which is activated by the protein or polypeptide product of the heterologous DNA molecule. The *R* gene can be naturally occurring in the plant

or heterologously inserted therein. A number of R genes have been identified in various plant species, including without limitation: *RPS2*, *RPM1*, and *RPP5* from *Arabidopsis thaliana*; *Cf2*, *Cf9*, *I2*, *Pto*, and *Prf* from tomato; *N* from tobacco; *L6* and *M* from flax; *Xa2l* from rice; and *Hs1pro-1* from sugar beet. In addition to imparting disease resistance, it is believed that stimulation of plant defenses in transgenic plants of the present invention will also result in a simultaneous enhancement in growth and resistance to insects.

According to another embodiment, a plant, transgenic or non-transgenic, is treated with a protein or polypeptide of the present invention. By treating, it is intended to include various forms of applying the protein or polypeptide to the plant. The embodiments of the present invention where the effector polypeptide or protein is applied to the plant can be carried out in a number of ways, including: 1) application of an isolated protein (or composition containing the same) or 2) application of bacteria which do not cause disease and are transformed with a gene encoding the effector protein of the present invention. In the latter embodiment, the effector protein can be applied to plants by applying bacteria containing the DNA molecule encoding the effector protein. Such bacteria are preferably capable of secreting or exporting the protein so that the protein can contact plant cells. In these embodiments, the protein is produced by the bacteria *in planta*.

Such topical application is typically carried out using an effector fusion protein which includes a transduction domain, which will afford transduction domain-mediated spontaneous uptake of the effector protein into cells. Basically, this is carried out by fusing an 11-amino acid peptide (YGRKKRRQRRR, SEQ. ID. No. 91) by standard rDNA techniques to the N-terminus of the effector protein, and the resulting tagged protein is taken up into cells by a poorly understood process. This peptide is the protein transduction domain (PTD) of the human immunodeficiency virus (HIV) TAT protein (Schwarze et al., 2000). Other PTDs are known and may possibly be used for this purpose (Prochiantz, 2000).

When the effector protein is topically applied to plants, it can be applied as a composition, which includes a carrier in the form, e.g., of water, aqueous solutions, slurries, or dry powders. In this embodiment, the composition contains greater than about 5 nM of the protein of the present invention.

Although not required, this composition may contain additional additives including fertilizer, insecticide, fungicide, nematicide, and mixtures thereof. Suitable fertilizers include $(NH_4)_2NO_3$. An example of a suitable insecticide is Malathion. Useful fungicides include Captan.

Other suitable additives include buffering agents, wetting agents, coating agents, and, in some instances, abrading agents. These materials can be used to facilitate the process of the present invention.

According to another aspect of the present invention, a transgenic plant is provided that contains a heterologous DNA molecule that encodes a transcript or a protein or polypeptide capable of disrupting function of a plant pathogen CEL product. Because the genes in the CEL are particularly important in pathogenesis, disrupting the function of their products in plants can result in broad resistance since CEL genes are highly conserved among Gram negative pathogens, particularly along species lines. An exemplary protein or polypeptide which can disrupt function of a CEL product is an antibody, polyclonal or monoclonal, raised against the CEL product using conventional techniques. Once isolated, the antibody can be sequenced and nucleic acids synthesized for encoding the same. Such nucleic acids, e.g., DNA, can be used to transform plants.

Transgenic plants can also be engineered so that they are hypersusceptible and, therefore, will support the growth of nonpathogenic bacteria for biotechnological purposes. It is known that many plant pathogenic bacteria can alter the environment inside plant leaves so that nonpathogenic bacteria can grow. This ability is presumably based on changes in the plant caused by pathogen effector proteins. Thus, transgenic plants expressing the appropriate effector genes can be used for these purposes.

According to one embodiment, a transgenic plant including a heterologous DNA molecule of the present invention expresses one or more effector proteins, wherein the transgenic plant is capable of supporting growth of compatible nonpathogenic bacteria (i.e., non-pathogenic endophytes such as various *Clavibacter* ssp.). The compatible nonpathogenic bacteria can be naturally occurring or it can be recombinant. Preferably, the nonpathogenic bacteria is recombinant and expresses one or more useful products. Thus, the transgenic plant becomes a green factory for

producing desirable products. Desirable products include, without limitation, products that can enhance the nutritional quality of the plant or products that are desirable in isolated form. If desired in isolated form, the product can be isolated from plant tissues. To prevent competition between the non-pathogenic bacteria which express the desired product and those that do not, it is possible to tailor the needs of recombinant, non-pathogenic bacteria so that only they are capable of living in plant tissues expressing a particular effector protein or polypeptide of the present invention.

The effector proteins or polypeptides of the present invention are believed to alter the plant physiology by shifting metabolic pathways to benefit the parasite and by activating or suppressing cell death pathways. Thus, they may also provide useful tools for efficiently altering the nutrient content of plants and delaying or triggering senescence. There are agricultural applications for all of these possible effects.

A further aspect of the present invention relates to diagnostic uses of the CEL and EEL. The CEL genes are universal to species of Gram negative bacteria, particularly pathogenic Gram negative bacteria (such as *P. syringae*), whereas the EEL sequences are strain-specific and provide a "virulence gene fingerprint" that could be used to track the presence, origins, and movement (and restrict the spread through quarantines) of strains that are particularly threatening. Although the CEL and EEL have been identified in various pathovars of *Pseudomonas syringae*, it is expected that most all Gram-negative pathogens can be identified, distinguished, and classified based upon the homology of the CEL and EEL genes.

According to one embodiment, a method of determining relatedness between two bacteria is carried out by comparing a nucleic acid alignment or amino acid alignment for a CEL of the two bacteria and then determining the relatedness of the two bacteria, wherein a higher sequence identity indicates a closer relationship. The CEL is particularly useful for determining the relatedness of two distinct bacterial species.

According to another embodiment, a method of determining relatedness between two bacteria which is carried out by comparing a nucleic acid alignment or amino acid alignment for an EEL of the two bacteria and then

determining the relatedness of the two bacteria, wherein a higher sequence identity indicates a closer relationship. The EEL is particularly useful for determining the relatedness of two pathovars of a single bacterial species.

Given the methods of determining relatedness of bacteria species and/or pathovars, these methods can be utilized in conjunction with plant breeding programs. By detecting the "virulence gene fingerprint" of pathogens which are prevalent in a particular growing region, it is possible either to develop transgenic cultivars as described above or to identify existing plant cultivars which are resistant to the prevalent pathogens.

In addition to the above described uses, another aspect of the present invention relates to gene- and protein-based therapies for animals, preferably mammals including, without limitation, humans, dogs, mice, rats. The *P. syringae* pv. *syringae* B728a EEL ORF5 protein (SEQ. ID. No. 32) is a member of the AvrRxv/YopJ protein family. YopJ is injected into human cells by the *Yersinia* type III secretion system, where it disrupts the function of certain protein kinases to inhibit cytokine release and promote programmed cell death. It is believed that the targets of many pathogen effector proteins (i.e., *P. syringae* effector proteins) will be universal to eukaryotes and therefore have a variety of potentially useful functions. In fact, two of the proteins in the *P. syringae* Hrp pathogenicity islands are toxic when expressed in yeast. They are HopPsyA from the *P. syringae* pv. *syringae* EEL and HopPtoA from the *P. syringae* pv. *tomato* DC3000 CEL. This supports the concept of universal eukaryote targets.

Thus, a further aspect of the present invention relates to a method of causing eukaryotic cell death which is carried out by introducing into a eukaryotic cell a cytotoxic *Pseudomonas* protein. The cytotoxic *Pseudomonas* protein is preferably HopPsyA (e.g., SEQ. ID. Nos. 36 (*Psy* 61), 62 (*Psy* 226), or 64 (*Psy* B143)) HopPtoA (SEQ. ID. No. 7), or HopPtoA2 (SEQ. ID. No. 66). The eukaryotic cell which is treated can be either *in vitro* or *in vivo*. When treating eukaryotic cells *in vivo*, a number of different protein- or DNA-delivery systems can be employed to introduce the effector protein into the target eukaryotic cell.

Without being bound by theory, it is believed that at least the HopPsyA effector proteins exert their cytotoxic effects through Mad2 interactions, disrupting cell checkpoint of spindle formation (see *infra*).

The protein- or DNA-delivery systems can be provided in the form of pharmaceutical compositions which include the delivery system in a pharmaceutically acceptable carrier, which may include suitable excipients or stabilizers. The dosage can be in solid or liquid form, such as powders, solutions, suspensions, or emulsions. Typically, the composition will contain from about 0.01 to 99 percent, preferably from about 20 to 75 percent of active compound(s), together with the carrier, excipient, stabilizer, etc.

The compositions of the present invention are preferably administered in injectable or topically-applied dosages by solution or suspension of these materials in a physiologically acceptable diluent with a pharmaceutical carrier. Such carriers include sterile liquids, such as water and oils, with or without the addition of a surfactant and other pharmaceutically and physiologically acceptable carrier, including adjuvants, excipients or stabilizers. Illustrative oils are those of petroleum, animal, vegetable, or synthetic origin, for example, peanut oil, soybean oil, or mineral oil. In general, water, saline, aqueous dextrose and related sugar solution, and glycols, such as propylene glycol or polyethylene glycol, are preferred liquid carriers, particularly for injectable solutions.

Alternatively, the effector proteins can also be delivered via solution or suspension packaged in a pressurized aerosol container together with suitable propellants, for example, hydrocarbon propellants like propane, butane, or isobutane with conventional adjuvants. The materials of the present invention also may be administered in a non-pressurized form such as in a nebulizer or atomizer.

Depending upon the treatment being effected, the compounds of the present invention can be administered orally, topically, transdermally, parenterally, subcutaneously, intravenously, intramuscularly, intraperitoneally, by intranasal instillation, by intracavitary or intravesical instillation, intraocularly, intraarterially, intralesionally, or by application to mucous membranes, such as, that of the nose, throat, and bronchial tubes.

Compositions within the scope of this invention include all compositions wherein the compound of the present invention is contained in an amount effective to achieve its intended purpose. While individual needs vary, determination of optimal ranges of effective amounts of each component is within the skill of the art.

One approach for delivering an effector protein into cells involves the use of liposomes. Basically, this involves providing a liposomc which includes that effector protein to be delivered, and then contacting the target cell with the liposome under conditions effective for delivery of the effector protein into the cell.

Liposomes are vesicles comprised of one or more concentrically ordered lipid bilayers which encapsulate an aqueous phase. They are normally not leaky, but can become leaky if a hole or pore occurs in the membrane, if the membrane is dissolved or degrades, or if the membrane temperature is increased to the phase transition temperature. Current methods of drug delivery via liposomes require that the liposome carrier ultimately become permeable and release the encapsulated drug at the target site. This can be accomplished, for example, in a passive manner wherein the liposome bilayer degrades over time through the action of various agents in the body. Every liposome composition will have a characteristic half-life in the circulation or at other sites in the body and, thus, by controlling the half-life of the liposome composition, the rate at which the bilayer dcgrades can be somewhat regulated.

In contrast to passive drug release, active drug release involves using an agent to induce a permeability change in the liposome vesicle. Liposome membranes can be constructed so that they become destabilized when the environment becomes acidic near the liposome membrane (see, e.g., Proc. Natl. Acad. Sci. USA 84:7851 (1987); Biochemistry 28:908 (1989), which are hereby incorporated by refcrence). When liposomes are endocytosed by a target cell, for example, they can be routed to acidic endosomes which will destabilize the liposome and result in drug release.

Alternatively, the liposome membrane can be chemically modified such that an enzyme is placed as a coating on the membrane which slowly destabilizes the liposome. Since control of drug release depends on the concentration of enzyme

initially placed in the membrane, there is no real effective way to modulate or alter drug release to achieve "on demand" drug delivery. The same problem exists for pH-sensitive liposomes in that as soon as the liposome vesicle comes into contact with a target cell, it will be engulfed and a drop in pH will lead to drug release.

This liposome delivery system can also be made to accumulate at a target organ, tissue, or cell via active targeting (e.g., by incorporating an antibody or hormone on the surface of the liposomal vehicle). This can be achieved according to known methods.

Different types of liposomes can be prepared according to Bangham et al., (1965); U.S. Patent No. 5,653,996 to Hsu et al., U.S. Patent No. 5,643,599 to Lee et al.; U.S. Patent No. 5,885,613 to Holland et al.; U.S. Patent No. 5,631,237 to Dzau et al.; and U.S. Patent No. 5,059,421 to Loughrey et al.

An alternative approach for delivery of effector proteins involves the conjugation of the desired effector protein to a polymer that is stabilized to avoid enzymatic degradation of the conjugated effector protein. Conjugated proteins or polypeptides of this type are described in U.S. Patent No. 5,681,811 to Ekwuribe.

Yet another approach for delivery of proteins or polypeptides involves preparation of chimeric proteins according to U.S. Patent No. 5,817,789 to Heartlein et al. The chimeric protein can include a ligand domain and, e.g., an effector protein of the present invention. The ligand domain is specific for receptors located on a target cell. Thus, when the chimeric protein is delivered intravenously or otherwise introduced into blood or lymph, the chimeric protein will adsorb to the targeted cell, and the targeted cell will internalize the chimeric protein, which allows the effector protein to de-stabilize the cell checkpoint control mechanism, affording its cytotoxic effects.

When it is desirable to achieve heterologous expression of an effector protein of the present invention in a target cell, DNA molecules encoding the desired effector protein can be delivered into the cell. Basically, this includes providing a nucleic acid molecule encoding the effector protein and then introducing the nucleic acid molecule into the cell under conditions effective to express the effector protein in the cell. Preferably, this is achieved by inserting the nucleic acid molecule into an expression vector before it is introduced into the cell.

When transforming mammalian cells for heterologous expression of an effector protein, an adenovirus vector can be employed. Adenovirus gene delivery vehicles can be readily prepared and utilized given the disclosure provided in Berkner, 1988, and Rosenfeld et al., 1991. Adeno-associated viral gene delivery vehicles can be constructed and used to deliver a gene to cells. The use of adeno-associated viral gene delivery vehicles *in vitro* is described in Chatterjee et al. 1992; Walsh et al. 1992; Walsh et al., 1994; Flotte et al., 1993a; Ponnazhagan et al., 1994; Miller et al., 1994; Einerhand et al., 1995; Luo et al., 1995; and Zhou et al., 1996. *In vivo* use of these vehicles is described in Flotte et al., 1993b and Kaplitt et al., 1994. Additional types of adenovirus vectors are described in U.S. Patent No. 6,057,155 to Wickham et al.; U.S. Patent No. 6,033,908 to Bout et al.; U.S. Patent No. 6,001,557 to Wilson et al.; U.S. Patent No. 5,994,132 to Chamberlain et al.; U.S. Patent No. 5,981,225 to Kochanek et al.; U.S. Patent No. 5,885,808 to Spooner et al.; and U.S. Patent No. 5,871,727 to Curiel.

Retroviral vectors which have been modified to form infective transformation systems can also be used to deliver nucleic acid encoding a desired effector protein into a target cell. One such type of retroviral vector is disclosed in U.S. Patent No. 5,849,586 to Kriegler et al.

Regardless of the type of infective transformation system employed, it should be targeted for delivery of the nucleic acid to a specific cell type. For example, for delivery of the nucleic acid into tumor cells, a high titer of the infective transformation system can be injected directly within the tumor site so as to enhance the likelihood of tumor cell infection. The infected cells will then express the desired effector protein, e.g., HopPtoA, HopPsyA, or HopPtoA2, disrupting cellular functions and producing cytotoxic effects.

Particularly preferred is use of the effector proteins of the present invention to treat a cancerous condition (i.e., the eukaryotic cell which is affected is a cancer cell). This can be carried out by introducing a cytotoxic *Pseudomonas* protein into cancer cells of a patient under conditions effective to inhibit cancer cell division, thereby treating the cancerous condition.

By introducing, it is intended that the effector protein is administered to the patient, preferably in the form of a composition which will target delivery to the

cancer cells. Alternatively, when using DNA-based therapies, it is intended that the introducing be carried out by administering a target DNA delivery system to the patient such that the cancer cells are targeted and the effector protein is expressed therein.

Examples

The following Examples are intended to be illustrative and in no way are intended to limit the scope of the present invention.

Materials and Methods

Bacterial Strains, Culture Conditions, Plasmids, and DNA Manipulation Techniques:

Three experimentally amenable strains that represent different levels of diversity in *P. syringae* were investigated: *Psy* 61, *Psy* B728a, and *Pto* DC3000. (i) *Psy* 61 is a weak pathogen of bean whose *hrp* gene cluster, cloned on cosmid pHIR11, contains all of the genes necessary for nonpathogenic bacteria like *Pseudomonas fluorescens* and *Escherichia coli* to elicit the HR in tobacco and to secrete in culture the HrpZ harpin, a protein with unknown function that is secreted abundantly by the Hrp system (Alfano et al., 1996). The pHIR11 *hrp* cluster has been completely sequenced (Figure 1) (Alfano and Collmer, 1997), and the *hopPsyA* gene in the hypervariable region at the left edge of the cluster was shown to encode a protein that has an Avr phenotype, travels the Hrp pathway, and elicits cell death when expressed in tobacco cells (Alfano and Collmer, 1997; Alfano et al., 1997; van Dijk et al., 1999). (ii) *Psy* B728a is in the same pathovar as strain 61 but is highly virulent and is a model for studying the role of the Hrp system in epiphytic fitness and pathogenicity (brown spot of bean) in the field (Hirano et al., 1999). (iii) *Pto* DC3000 is a well-studied pathogen of Arabidopsis and tomato (causing bacterial speck) that is highly divergent from pathovar syringae strains. Analysis of rRNA operon RFLP patterns has indicated that *Pto* and *Psy* are distantly related and could be considered separate species (Manceau and Horvais, 1997). Thus, we were able to compare two strains in the same pathovar with a strain from a highly divergent pathovar.

Conditions for culturing *E. coli* and *P. syringae* strains have been described (van Dijk et al., 1999), as have the sources for *Psy* 61 (Preston et al., 1995), *Psy* B728a (Hirano et al., 1999), and *Pto* DC3000 (Preston et al., 1995). Cloning and DNA manipulations were done in *E. coli* DH5α using pBluescript II (Stratagene, La Jolla, CA), pRK415 (Keen et al., 1988), and cosmid pCPP47 (Bauer and Collmer, 1997), according to standard procedures (Ausubel et al., 1994). Cosmid libraries of *Pto* DC3000 and *Psy* B728a genomic DNA were previously constructed (Charkowski et al., 1998). Oligonucleotide synthesis and DNA sequencing were performed at the Cornell Biotechnology Center. The nucleotide sequence of the *Pto* DC3000 *hrp/hrc* cluster was determined using subclones of pCPP2473, a cosmid selected from a genomic cosmid library based on hybridization with the *hrpK* gene of *Psy* 61. The nucleotide sequence of the *Psy* B728a *hrp/hrc* cluster was determined using subclones of pCPP2346 and pCPP3017. These cosmids were selected from a genomic library based on hybridization with the *hrpC* operon of 61. The left side of the *Psy* 61 EEL region was cloned by PCR into pBSKSII+ *Xho*I and *Eco*RI sites using the following primers:

SEQ. ID. NO. 71, which primes within *queA* and contains an *Xho*I site:

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atgactcgag gcgtggattc aggcaaat                                    28
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SEQ. ID. NO. 72, which primes within *hopPsyA* and contains an *Eco*RI site:

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atgagaattc tgccgccgct ttctcgtt                                    28
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Pfu polymerase was used for all PCR experiments. DNA sequence data were managed and analyzed with the DNAStar Program (Madison, WI), and databases were searched with the BLASTX, BLASTP, and BLASTN programs (Altschul et al., 1997).

Mutant Construction and Analysis:

Large deletions in the *Pto* DC3000 Hrp Pai were constructed by subcloning border fragments into restriction sites on either side of an ΩSp^R cassette in pRK415, electroporating the recombinant plasmids into DC3000, and then selecting and screening for marker exchange mutants as described (Alfano et al., 1996). The

following left and right side (Figures 2 and 3) deletion border fragments were used (with residual gene fragments indicated): for CUCPB5110 left *tgt-gueA*-tRNA-^{Leu} - ORF4' (27 bp of ORF4) and right ORF1'-*hrpK* (396 bp of ORF1); and for CUCPB5115 left *hrpS'-avrE'* (2569 bp of *avrE*) and right ORF6 (156 bp upstream of ORF6 start codon). The later fragment was PCR-amplified using the following primers:

SEQ. ID. NO. 73, which primes in the ORF5-ORF6 intergenic region and contains an *Xba*I site:

cgctctagac caaggactgc 20

SEQ. ID. NO. 74, which primes in ORF6 and contains a *Hind*III site:

ccagaagctt ctgtttttga gtc 23

Mutant constructions were confirmed by Southern hybridizations using previously described conditions (Charkowski et al., 1998). The ability of mutants to secrete AvrPto was determined with anti-AvrPto antibodies and immunoblot analysis of cell fractions as previously described (van Dijk et al., 1999). Mutant CUCPB5115 was complemented with pCPP3016, which carries ORF2 through ORF10 in cosmid pCPP47, and was introduced from *E. coli* DH5α by triparental mating using helper strain *E. coli* DH5α(pRK600), as described (Charkowski et al., 1998).

T7 Expression Analysis:

Protein products of the *Pto* DC3000 EEL were analyzed by T7 polymerase-dependent expression using vector pET21 and *E. coli* BL21(DE3) as previously described (Huang et al., 1995). The following primer sets were used to PCR each ORF from pCPP3091, which carries in pBSKSII+ a *Bam*H1 fragment containing *tgt* to *hrcV*:

ORF1, SEQ. ID. Nos. 75 and 76, respectively:

agtaggatcc tgaaatgtag gggcccgg 28

agtaaagctt atgatgctgt ttccagta 28

ORF2, SEQ. ID. Nos. 77 and 78, respectively:

agtaggatcc tctcgaagga atggagca 28

agtaaagctt cgtgaagatg catttcgc 28

ORF3, SEQ. ID. Nos. 79 and 80, respectively:

agtaggatcc tagtcactga tcgaacgt 28

agtactcgag ccacgaaata acacggta 28

ORF4, SEQ. ID. Nos. 81 and 82, respectively:

agtaggatcc caggactgcc ttccagcg 28

agtactcgag cagagcggcg tccgtggc 28

tnpA, SEQ. ID. Nos. 83 and 84, respectively:

agtaggatcc agaattgttg aagaaatc 28

agtaaagctt tgcgctgtta actcatcg 28

Plant Bioassays:

Tobacco (*Nicotiana tabacum* L. cv. Xanthi) and tomato (*Lycopersicon esculentum* Mill. cvs. Moneymaker and Rio Grande) were grown under greenhouse conditions and then maintained at 25°C with daylight and supplemental halide illumination for HR and virulence assays. Bacteria were grown overnight on King's medium B agar supplemented with appropriate antibiotics, suspended in 5 mM MES pH 5.6, and then infiltrated with a needleless syringe into the leaves of test plants at 10^8 cfu/ml for HR assays and 10^4 cfu/ml for pathogenicity assays (Charkowski et al., 1998). All assays were repeated at least four times on leaves from different plants. Bacterial growth in tomato leaves was assayed by excising disks from infiltrated areas with a cork borer, comminuting the tissue in 0.5 ml of 5 mM MES, pH 5.6, with a Kontes Pellet Pestle (Fisher Scientific, Pittsburgh, PA), and then dilution plating the homogenate on King's medium B agar with 50 µg/ml rifampicin and 2 µg/ml cycloheximide to determine bacterial populations. The mean and SD from three leaf samples were determined for each time point. The relative growth in planta of DC3000 and CUCPB5110 was similarly assayed in 4 independent experiments and the relative growth of DC3000, CUCPB5115, and CUCPB5115(pCPP3016) in 3 independent experiments. Although the final population levels achieved by DC3000 varied between experiments, the

populations levels of the mutants relative to the wild type were the same as in the representative experiments presented below.

Example 1 - Comparison of *hrp/hrc* Gene Clusters of *Psy* 61, *Psy* B728a, and *Pto* DC3000

To determine if the *hrp/hrc* clusters from *Psy* B728a and *Pto* DC3000 were organized similarly to the previously characterized *hrp/hrc* cluster of *Psy* 61, two cosmids carrying *hrp/hrc* inserts were partially characterized. pCPP2346 carries the entire *hrp/hrc* cluster of B728a, and pCPP2473 carries the left half of the *hrp/hrc* cluster of DC3000. The right half of the DC3000 *hrp/hrc* cluster had been characterized previously (Preston et al., 1995). Sequencing the ends of several subclones derived from these cosmids provided fingerprints of the B728a and DC3000 *hrp/hrc* clusters, which indicated that both are arranged like that of strain 61 (Fig. 1). However, B728a contains between *hrcU* and *hrpV* a 3.6-kb insert with homologs of bacteriophage lambda genes Ea59 (23% amino-acid identity; $E = 2e\text{-}7$) and Ea31 (30% amino-acid identity; $E = 6e\text{-}8$) (Hendrix et al., 1983), and the B728a *hrcU* ORF has 36 additional codons. A possible insertion of this size in several *Psy* strains that are highly virulent on bean was suggested by a previous RFLP analysis (Legard et al., 1993). Cosmid pCPP2346, which contains the B728a *hrp/hrc* region and flanking sequences (4 kb on the left and 13 kb on the right), enabled *P. fluorescens* to secrete the B728a HrpZ harpin in culture and to elicit the HR in tobacco leaves, however, confluent necrosis developed more slowly than with *P. fluorescens*(pHIR11) (data not shown). To further test the relatedness of the *Psy* 61 and B728a *hrp/hrc* gene clusters using an internal reference, the B728a *hrpA* gene was sequenced. Of the *hrp/hrc* genes that have been sequenced in *Psy* and *Pto*, *hrpA*, which encodes the major subunit of the Hrp pilus (Roine et al., 1997), is the least conserved (28% amino-acid identity) (Preston et al., 1995). However, the *hrpA* genes of strains 61 and B728a were 100% identical, which further supports the close relationship of these strains and their Hrp systems.

Example 2 - Identification of an Exchangeable Effector Locus (EEL) in the Hrp Pai between *hrpK* and tRNA^{Leu}

Sequence analysis of the left side of the *Psy* 61, *Psy* B728a, and *Pto* DC3000 Hrp Pais revealed that the high percentage identity in *hrpK* sequences in these strains abruptly terminates three nucleotides after the *hrpK* stop codon and then is restored near tRNA^{Leu}, *queA*, and *tgt* sequences after 2.5 kb (*Psy* 61), 7.3 kb (*Psy* B728a), or 5.9 kb (*Pto* DC3000) of dissimilar, intervening DNA (Figure 2). The difference between *Psy* strains 61 and B728a in this region was particularly surprising. This region of the *P. syringae* Hrp Pai was given the EEL designation because it contained completely different effector protein genes (Table 1 below), which appear to be exchanged at this locus at a high frequency. In this regard, it is noteworthy that (i) ORF2 in the B728a EEL is a homolog of *avrPphE*, which is in a different location, immediately downstream of *hrpK* (*hrpY*), in *Pph* 1302A (Mansfield et al., 1994), (ii) *hopPsyA* (*hrmA*) is present in only a few *Psy* strains (Heu and Hutcheson, 1993; Alfano et al., 1997), (iii) and ORF5 in the B728a EEL predicts a protein that is similar to *Xanthomonas* AvrBsT and possesses multiple motifs characteristic of the AvrRxv family (Ciesiolka et al., 1999). G+C content different from the genomic average is a hallmark of horizontally transferred genes, and the G + C contents of the ORFs in the three EELs are considerably lower than the average of 59-61% for *P. syringae* (Palleroni et al., 1984) (Table 1 below). They are also lower than *hrpK* (60%) and *queA* (63-64%). The ORFs in the *Pto* DC3000 EEL predict no products with similarity to known effector proteins, however T7 polymerase-dependent expression revealed products in the size range predicted for ORF1, ORF3, and ORF4. Furthermore, the ORF1 protein is secreted in a *hrp*-dependent manner by *E. coli*(pCPP2156), which expresses an *Erwinia chrysanthemi* Hrp system that secretes *P. syringae* Avr proteins (Ham et al., 1998). Several ORFs in these EELs are preceded by Hrp boxes indicative of HrpL-activated promoters (Figure 1) (Xiao and Hutcheson, 1994), and the lack of intervening Rho-independent terminator sequences or promoters suggests that ORF1 in DC3000 and ORF1 and ORF2 in B728a are expressed from HrpL-activated promoters upstream of the respective *hrpK* genes.

The EELs of these three strains also contain sequences homologous to insertion sequences, transposases, phage integrase genes, and plasmids (Figure 2 and Table 1 below). The *Psy* B728a ORF5 and ORF6 operon is bordered on the left side

by sequences similar to those in a *Pph* plasmid that carries several *avr* genes (Jackson et al., 1999) and by a sequence homologous to insertion elements that are typically found on plasmids, suggesting plasmid integration via an IS element in this region (Szabo and Mills, 1984). *Psy* B728a ORF3 and ORF4 show similarity to sequences implicated in the horizontal acquisition of the LEE Pai by pathogenic *E. coli* strains (Perna et al., 1998). These *Psy* B728a ORFs are not preceded by Hrp boxes and are unlikely to encode effector proteins.

Table 1: ORFs and fragments of genetic elements in the EELs of *Pto* DC3000, *Psy* B728a, and *Psy* 61 and similarities with known *avr* genes and mobile genetic elements.

ORF or sequence	% G+C	Size	BLAST *E* value with representative similar sequence(s) in database, or relevant feature
Pto DC3000[a]			
ORF1	55	466 aa	Hrp-secreted (Alfano, unpublished)
TnpA'	55	279 aa	1e-125 *P. stutzeri* TnpA1 (Bosch et al., 1999)
ORF2	51	241 aa	None
ORF3	53	138 aa	None
ORF4	47	136 aa	None
Psy B728a			
ORF1	51	323 aa	9e-40 *Pph* AvrPphC (Yucel et al., 1994)
ORF2	58	382 aa	1e-154 *Pph* AvrPphE (Mansfield et al., 1994)
ORF3	55	507 aa	2e-63 *E. coli* L0015 (Perna et al., 1998)
ORF4	55	118 aa	9e-9 *E. coli* L0014 (Perna et al., 1998)
ORF5	49	411 aa	1e-4 *Xcv* AvrBsT (Ciesiolka et al., 1999)
ORF6	52	120 aa	None
B plasmid	46	96 nt	1e-25 *Pph* pAV511 (Jackson et al., 1999)
IntA'	59	49 aa	3e-5 *E. coli* CP4-like integrase (Perna et al., 1998)
Psy 61			
HopPsyA	53	375 aa	Hrp-secreted Avr (Alfano et al., 1997; van Dijk et al., 1999)
ShcA	57	112 aa	6e-4 Y0008 (Perry et al., 1998)

[a] Pathovar abbreviations correspond to the recommendations of Vivian and Mansfield (1993) for uniform *avr* nomenclature.

The left border of the EELs contains sequences similar to many $tRNA^{Leu}$ genes and to *E. coli queA* and *tgt* queuosine biosynthesis genes (ca. 70% amino-acid identity in predicted products). The EEL sequences terminate at the 3' end of the *P. syringae* tRNA sequences, as is typical for Pais (Hou, 1999). Virtually identical *tgt-queA*-$tRNA^{Leu}$ sequences are found in the genome of *P. aeruginosa* PAO1 (www.pseudomonas.com), which is also in the fluorescent pseudomonad group. But PAO1 is not a plant pathogen, and this $tRNA^{Leu}$ in *P. aeruginosa* is not

linked to any type III secretion system genes or other genes in the Hrp Pai (Figure 2). Thus, this is the apparent point of insertion of the Hrp Pai in the ancestral *Pseudomonas* genome.

Example 3 - Identification of a Conserved Effector locus (CEL) Located on the Right Side of the Hrp Pai in *Psy* B728a and *Pto* DC3000

Previous studies of the region to the right of *hrpR* in DC3000 had revealed the existence of the *avrE* locus, which is comprised of two transcriptional units (Lorang and Keen, 1995), the 5' sequences for the first 4 transcriptional units beyond *hrpR* (Lorang and Keen, 1995), and the identity of the fourth transcriptional unit as the *hrpW* gene encoding a second harpin (Charkowski et al., 1998). The DNA sequence of the first 14 ORFs to the right of *hrpR* in *Pto* DC3000 was completed in this investigation and the corresponding region in *Psy* B728a was partially sequenced (Figure 3). Like the EEL, this region contains putative effector genes, e.g., *avrE* (Lorang and Keen, 1995). Unlike the EEL, the ORFs in this region have an average G + C content of 58.0% , which is close to that of the *hrp/hrc* genes, the region contains no sequences similar to known mobile genetic elements, and it appears conserved between *Psy* and *Pto* (Figure 3). Comparison of the regions sequenced in B728a and DC3000 revealed that the first 7 ORFs are arranged identically and have an average DNA sequence identity of 78%. Hence, this region was given the CEL designation.

The precise border of the CEL remains undefined, and no sequences that were repeated in the EEL border of the Hrp Pai were found. ORF7 and ORF8 are likely to be part of tbe CEL, based on the presence of an upstream Hrp box (Figure 3). However, the region beyond ORF10 probably is not in the CEL because the product of thc next ORF shows homology to a family of bacterial GstA proteins (e.g., 28% identity with *E. coli* GstA over 204 amino acids; *E* = 1e-8)(Blattner et al., 1997), and glutathione-*S*-transferase activity is common in nonpathogenic fluorescent pseudomonads (Zablotowicz et al., 1995). The presence of a *galP* homolog (38% identity over 256 amino acids, based on incomplete sequence, to *E. coli* GalP; E = 2e-42) (Blattner et al., 1997) in this region further suggests that it is beyond the CEL.

Several other features of this region in B728a and DC3000 are noteworthy. (i) Both strains have a 1-kb intergenic region between *hrpR* and ORF1

that is distinguished by low sequence identity (44%) but which contains three inverted repeats that could form stem loop structures affecting expression of the *hrpRS* operon. (ii) ORF1 is most similar to *E. coli* murein lytic transglycosylase MltD (38% identity over 324 amino acids; $E = 4e\text{-}56$). (iii) ORF2 is 42% identical over 130 amino acids with *E. amylovora* DspF ($E = 9e\text{-}24$), a candidate chaperone (Bogdanove et al., 1998a; Gaudriault et al., 1997). (iv) The ORF5 protein is secreted in a *hrp*-dependent manner by *E. coli*(pCPP2156), but mutation with an ΩSp^r cassette has little effect on either HR elicitation in tobacco or pathogenicity in tomato (Charkowski, unpublished). (v) Finally, six operons in this region are preceded by Hrp boxes (Lorang and Keen, 1995) (Figure 3), which is characteristic of known *avr* genes in *P. syringae* (Alfano et al., 1996). Thus, the CEL carries multiple candidate effectors.

Example 4 - Investigation of EEL and CEL Roles in Pathogenicity

A mutation was constructed in DC3000 that replaced all of the ORFs between *hrpK* and $tRNA^{Leu}$ (EEL) with an ΩSp^r cassette (Figure 2). This *Pto* mutant, CUCPB5110, was tested for its ability to elicit the HR in tobacco and to cause disease in tomato. The mutant retained the ability to elicit the HR and to produce disease symptoms, but it failed to reach population levels as high as the parental strain in tomato (Figure 4A).

A mutation was constructed in DC3000 that replaced *avrE* through ORF5 (CEL) with an ΩSp^r cassette. This deleted all of the CEL ORFs that were both partially characterized and likely to encode effectors. This *Pto* mutant, CUCPB5115, still elicited the HR in tobacco, but tissue collapse was delayed ca. 5 h (Figure 4C). The mutant no longer elicited disease symptoms in tomato when infiltrated at a concentration of 10^4 cfu/ml, and growth *in planta* was strongly reduced (Figure 4B). However, the mutant elicited an HR dependent on the tomato *Pto R* gene that was indistinguishable from the wild-type in tests involving PtoS (susceptible) and PtoR (resistant) Rio Grande tomato lines. Plasmid pCPP3016, which carries ORF2 through ORF10, fully restored the ability of CUCPB5115 to cause disease symptoms and partially restored the ability of the mutant to multiply in tomato leaves (Figures 4B and 4E). Deletion of the *hrp/hrc* cluster abolishes HR and pathogenicity phenotypes in *Pto* DC3000 (Collmer et al., 2000). To confirm that the large deletions in *Pto*

mutants CUCPB5110 and CUCPB5115 did not disrupt Hrp secretion functions, we compared the ability of these mutants, the DC3000 *hrp/hrc* deletion mutant, and wild-type DC3000 to make and secrete AvrPto in culture while retaining a cytoplasmic marker comprised of β-lactamase lacking its signal peptide. AvrPto provided an ideal subject for this test because it is a well-studied effector protein that is secreted in culture and injected into host cells *in planta* (Alfano and Collmer, 1997; van Dijk et al., 1999). Only the *hrp/hrc* deletion cluster mutant was impaired in AvrPto production and secretion (Figure 5).

Based on the above studies, the *P. syringae hrp/hrc* genes are part of a Hrp Pai that has three distinct loci: an EEL, the *hrp/hrc* gene cluster, and a CEL. The EEL harbors exchangeable effector genes and makes only a quantitative contribution to parasitic fitness in host plants. The *hrp/hrc* locus encodes the Hrp secretion system and is required for effector protein delivery, parasitism, and pathogenicity. The CEL makes no discernible contribution to Hrp secretion functions but contributes strongly to parasitic fitness and is required for *Pto* pathogenicity in tomato. The Hrp Pai of *P. syringae* has several properties of Pais possessed by animal pathogens (Hacker et al., 1997), including the presence of many virulence-associated genes (several with relatively low G+C content) in a large (ca. 50-kb) chromosomal region linked to a tRNA locus and absent from the corresponding locus in a closely related species. In addition, the EEL portion of the Hrp Pai is unstable and contains many sequences related to mobile genetic elements.

The EEL is a novel feature of known Pais, which is likely involved in fine-tuning the parasitic fitness of *P. syringae* strains with various plant hosts. By comparing closely- and distantly-related strains of *P. syringae*, we were able to establish the high instability of this locus and the contrasting high conservation of its border sequences. No single mechanism can explain the high instability, as we found fragments related to phages, insertion sequences, and plasmids in the *Psy* and *Pto* EELs, and insertion sequences were recently reported in the corresponding region of three other *P. syringae* strains (Inoue and Takikawa, 1999). The mechanism or significance of the localization of the EELs between $tRNA^{Leu}$ and *hrpK* sequences in the Hrp Pais also is unclear. *Pto* DC3000 carries at least one other effector gene, *avrPto*, that is located elsewhere in the genome (Ronald et al., 1992), many

P. syringae avr genes are located on plasmids (Leach and White, 1996), and the EEL ORFs represent a mix of widespread, (e.g., *avrRxv* family) and seemingly rare (e.g., *hopPsyA*), effector genes. The G + C content of the EEL ORFs is significantly lower than that of the rest of the Hrp Pai and the *P. syringae* genome. Although certain genes in the non-EEL portions of the Hrp Pai, such as *hrpA*, are highly divergent, they have a high G + C content, and there is no evidence that they have been horizontally transferred separately from the rest of the Hrp Pai. The relatively low G + C content of the ORFs in the EELs (and of other *P. syringae avr* genes) suggests that these genes may be horizontally acquired from a wider pool of pathogenic bacteria than just *P. syringae* (Kim et al., 1998). Indeed, the *avrRxv* family of genes is found in a wide range of plant and animal pathogens (Ciesiolka et al., 1999). The weak effect on parasitic fitness of deleting the *Pto* DC3000 EEL, or of mutating *hopPsyA* (*hrmA*) in *Psy* 61 (Huang et al., 1991), is typical of mutations in individual *avr* genes and presumably results from redundancy in the effector protein system (Leach and White, 1996).

The functions of *hrpK* and of the CEL ORF1 are unclear but warrant discussion. These two ORFs reside just outside the *hrpL* and *hrpR* delimited cluster of operons containing both *hrp* and *hrc* genes and thereby spatially separate the three regions of the Hrp Pai (Figures 1-3). *hrpK* mutants have a variable Hrp phenotype (Mansfield et al., 1994; Bozso et al., 1999), and a *Psy* B728a *hrpK* mutant still secretes HrpZ (Alfano, unpublished), which suggests that HrpK may be an effector protein. Nevertheless, the HrpK proteins of *Psy* 61 and *Pto* DC3000 are 79% identical and therefore are more conserved than many Hrp secretion system components. It is also noteworthy that *hrpK* appears to be in an operon with other effector genes in *Psy* B728a and *Pto* DC3000. In contrast, the CEL ORF1 may contribute (weakly or redundantly) to Hrp secretion functions by promoting penetration of the system through the bacterial peptidoglycan layer. The ORF1 product has extensive homology with *E. coli* MltD and shares a lysozyme-like domain with the product of *ipgF* (Mushegian et al., 1996), a *Shigella flexneri* gene that is also located between loci encoding a type III secretion system and effector proteins (Allaoui et al., 1993). Mutations in these genes in *Pto* and *S. flexneri* have no

obvious phenotype (Lorang and Keen, 1995; Allaoui et al., 1993), as is typical for genes encoding peptidoglycan hydrolases (Dijkstra and Keck, 1996).

The loss of pathogenicity in *Pto* mutant CUCPB5115, with an *avrE*-ORF5 deletion in the CEL, was surprising because pathogenicity is retained in DC3000 mutants in which the corresponding operons are individually disrupted (Lorang and Keen, 1995; Charkowski et al., 1998). In assessing the possible function of this region and the conservation of its constituent genes, it should be noted that *avrE* is unlike other *avr* genes found in *Pto* in that it confers avirulence to *P. syringae* pv glycinea on all tested soybean cultivars and it has a homolog (*dspE*) in *E. amylovora* that is required for pathogenicity (Lorang and Keen, 1995; Bogdanove et al., 1998b). Although the CEL is required for pathogenicity, it is not essential for type III effector protein secretion because the mutant still secretes AvrPto. It also appears to play no essential role in type III translocation of effector proteins into plant cells because the mutant still elicits the HR in nonhost tobacco and in a PtoR-resistance tomato line, and pHIR11, which lacks this region, appears capable of translocating several Avr proteins (Gopalan et al., 1996; Pirhonen et al., 1996). The conservation of this region in the divergent pathovars *Psy* and *Pto*, and its importance in disease, suggests that the products of the CEL may be redundantly involved in a common, essential aspect of pathogenesis.

The similar G + C content and codon usage of the *hrp/hrc* genes, the genes in the CEL, and total *P. syringae* genomic DNA suggests that the Hrp Pai was acquired early in the evolution of *P. syringae*. Although, the EEL region may have similarly developed carly in the radiation of *P. syringae* into its many pathovars, races, and strains, the apparent instability that is discussed above suggests ongoing rapid evolution at this locus. Indeed, many *P. syringae avr* genes are associated with mobile genetic elements, regardless of their location (Kim et al., 1998). Thus, it appears that Hrp-mediated pathogenicity in *P. syringae* is collectively dependent on a set of genes that are universal among divergent pathovars and on another set that varies among strains even in the same pathovar. The latter are presumably acquired and lost in response to opposing selection pressures to promote parasitism while evading host *R*-gene surveillance systems.

Example 5 - Role of ShcA as a Type III Chaperone for the HopPsyA Effector

The ORF upstream of *hopPsyA*, tentatively named *shcA*, encodes a protein product of the predicted molecular mass. The ORF upstream of the *hopPsyA* gene in *P. s. syringae* 61 (originally designated ORF1) shares sequence identity with *exsC* and ORF7, which are genes adjacent to type III effector genes in *P. aeruginosa* and *Yersinia pestis*, respectively (Frank and Iglewski, 1991; Perry et al., 1998). Although neither of these ORFs have been shown experimentally to encode chaperones, they have been noted to share properties that type III chaperones often possess (Cornellis et al., 1998). One of these properties is the location of the chaperone gene itself (Figures 1 and 6). Chaperone genes are often adjacent to a gene that encodes the effector protein with which the chaperone interacts. Furthermore, *shcA* also shares other common characteristics of type III chaperones: its protein product is relatively small (about 14 kDa), it has an acidic pI, and it has a C-terminal region that is predicted to be an amphipathic α-helix. To begin assessing the function of *shcA*, it was first determined whether *shcA* encodes a protein product. A construct was prepared using PCR that fused *shcA* in-frame to a sequence encoding the FLAG epitope. This construct, pLV26, contains the nucleotide sequence upstream of *shcA*, including a putative ribosome binding site (RBS). DH5αF'IQ(pLV26) cultures were grown in rich media and induced at the appropriate density with IPTG. Whole cell lysates were separated by SDS-PAGE and analyzed with immunoblots using anti-FLAG antibodies. By comparing the ShcA-FLAG encoded by pLV26 to a construct that made ShcA-FLAG from a vector RBS, it was concluded that the native RBS upstream of *shcA* was competent for translation (Figure 7). Thus, the *shcA* ORF is a legitimate gene that encodes a protein product.

To test the effects of *shcA* on bacterial-plant interactions, an *shcA* mutation was constructed in the minimalist *hrp/hrc* cluster carried on cosmid pHIR11. There are distinct advantages to having the *shcA* mutation marker-exchanged into pHIR11. The main one is that the HR assay can be used as a screen to determine if HopPsyA is being translocated into plant cells because the pHIR11-dependent HR requires the delivery of HopPsyA into plant cells (Alfano et al., 1996; Alfano et al., 1997). With the chromosomal *shcA* mutant, other Hop proteins would probably be delivered to the interior of plant cells. Some of these proteins would be recognized by

the *R* gene-based plant surveillance system and initiate an HR masking any defect in HopPsyA delivery. *E. coli* MC4100 carrying pLV10, a pHIR11 derivative, which contains a nonpolar *nptII* cartridge within *shcA*, was unable to elicit an HR on tobacco (Figure 8). This indicates that *shcA* is required for the translocation of HopPsyA into plant cells. To determine if HopPsyA was secreted in culture, cultures of the nonpathogen *P. fluorescens* 55 were grown. This bacterium carried either pHIR11, pCPP2089 (a pHIR11 derivative defective in type III secretion), or pLV10. The representative results can be seen in Figure 8. *shcA* was required for the in-culture type III secretion of the HopPsyA effector protein, but not for HrpZ secretion, another protein secreted by the pHIR11 encoded Hrp system. These results indicate that the defect in type III secretion is specific to HopPsyA and are consistent with *shcA* encoding a chaperone for HopPsyA. It was after these results that the ORF upstream of the *hopPsyA* gene was named *shcA* for specific hop chaperone for HopPsyA, a naming system consistent with the naming system researchers have employed for chaperones in the archetypal *Yersinia* type III system.

Example 6 - Cytotoxic Effects of *hopPsyA* Expressed in Plants

Transient expression of *hopPsyA* DNA *in planta* induces cell death in *Nicotiana tabacum*, but not in *N. benthamiana*, bean, or in *Arabidopsis*. To determine whether HopPsyA induced cell death on tobacco leaves as it did when produced in tobacco suspension cells, a transformation system that delivers the *hopPsyA* gene on T-DNA of *Agrobacterium tumefaciens* was used (Rossi et al., 1993; van den Ackerveken et al., 1996). This delivery system works better than biolistics for transiently transforming whole plant leaves. For these experiments, vector pTA7002, kindly provided by Nam-Hai Chua and his colleagues at Rockefeller University, was used. The unique property of this vector is that it contains an inducible expression system that uses the regulatory mechanism of the glucocorticoid receptor (Picard et al., 1988; Aoyama and Chua, 1997; McNellis et al., 1998). pTA7002 encodes a chimeric transcription factor consisting of the DNA-binding domain of GAL4, the transactivating domain of the herpes viral protein VP16, and the receptor domain of the rat glucocorticoid receptor. Also contained on this vector is a promoter containing GAL4 upstream activating sequences (UAS) upstream of a multiple cloning site.

Thus, any gene cloned downstream of the promoter containing the GAL4-UAS is induced by glucocorticoids, of which a synthetic glucocorticoid, dexamethasone (DEX), is available commercially. *hopPsyA* was PCR-cloned downstream of the GAL4-UAS. Plant leaves from several different test plants were infiltrated with *Argrobacterium* carrying pTA7002::*hopPsyA* and after 48 hours these plants were sprayed with DEX. Only *N. tabacum* elicited an HR in response to the DEX-induced transient expression of *hopPsyA* (Figure 13A). In contrast, *N. benthamiana* produced no obvious response after DEX induction (Figure 13B). Moreover, transient expression of *hopPsyA* in bean plants (*Phaseolus vulgaris* L. 'Eagle')(data not shown) and *Arabidopsis thaliana* ecotype Col-1 (Figure 13) did not result in a HR. These results suggest that bean cv. Eagle, *Arabidopsis* Col-1, and *N. benthamiana* lack a resistance protein that can recognize HopPsyA. The lack of an apparent defense response for HopPsyA transiently expressed in bean was predicted, because HopPsyA is normally produced in *P. s. syringae* 61, a pathogen of bean. But, it was somewhat unknown how transient expression of HopPsyA would effect *Arabidopsis*. However, since *P. s. tomato* DC3000, a pathogen of *Arabidopsis*, appears to have a *hopPsyA* homolog based on DNA gel blots using *hopPsyA* as a probe, it was expected that HopPsyA would not to be recognized by an R protein in *Arabidopsis* (i.e., no HR produced) (Alfano et al., 1997). Thus, these plants (bean, *Arabidopsis*, and *N. benthamiana*) should represent ideal plants to explore the bacterial-intended role of HopPsyA in plant pathogenicity.

P.s. pv. *syringae* 61 secretes HopPsyA in culture via the Hrp (type III) protein secretion system. Because the *P. syringae* Avr proteins AvrB and AvrPto were found to be secreted by the type III secretion system encoded by the functional *E. chrysanthemi hrp* cluster carried on cosmid pCPP2156 expressed in *E. coli* (Ham et al., 1998), detection of HopPsyA secretion in culture directly via the native Hrp system carried in *P. s. syringae* 61 was tested. *P. s. syringae* 61 cultures grown in *hrp*-derepressing fructose minimal medium at 22°C were separated into cell-bound and supernatant fractions by centrifugation. Proteins present in the supernatant fractions were concentrated by TCA precipitation, and the cell-bound and supernatant samples were resolved with SDS-PAGE and analyzed with immunoblots using anti-HopPsyA antibodies. A HopPsyA signal was detected in supernatant fractions from

wild type *P. s. syringae* 61 (Figure 14). Importantly, HopPsyA was not detected in supernatant fractions from *P. s. syringae* 61-2089, which is defective in Hrp secretion, indicating that the HopPsyA signal in the supernatant was due specifically to type III protein secretion (Figure 14). As a second control, both strains contained pCPP2318, which encodes the mature β-lactamase lacking its N-terminal signal pcptide, and provides a marker for cell lysis. β-lactamase was detected only in the cell-bound fractions of these samples, clearly showing that cell lysis did not occur at a significant level (Figure 14). The fact that HopPsyA is secreted via the type III secretion system in culture and that the avirulence activity of HopPsyA occurs only when it is expressed in plant cells strongly support that HopPsyA is delivered into plant cells via the type III pathway.

HopPsyA contributes in a detectable, albeit minor, way to growth of *P. s. syringae* 61 in bean. The effect of a HopPsyA mutation on the multiplication of *P. s. syringae* 61 in bean tissue has been reported (Huang et al., 1991). These data essentially indicate that HopPsyA contributes little to the ability of *P. s. syringae* 61 to multiply in bean. The *P. s. syringae* 61 *hopPsyA* mutant does not grow as well in bean leaves as the wild-type strain (Figure 15). This was unexpected, because these results are in direct conflict with previously reported data. One rationale for the discrepancy is that the previous reports focused primarily on the major phenotype that a *hrp* mutant exhibits on *in planta* growth and predated the discovery that HopPsyA was a type III-secreted protein. Thus, it is quite possible that the earlier experiments missed the morc subtle effect that HopPsyA appears to have on the multiplication of *P. s. syringae* 61 in bean tissue (Huang et al., 1991). The data presented here supports that HopPsyA contributes to the pathogenicity of *P. s. syringae* and are consistent with the hypothesis that the majority of Hops from *P. syringae* contribute subtly to pathogenicity. The lack of strong pathogenicity phenotypes for mutants defective in different *avr* and *hop* genes may be due to possible *avr/hop* gene redundancy or a decreased dependence on any one Hop protein through coevolution with the plant. Indeed, the type III-delivered proteins of plant pathogens that are delivered into plant cells may not be virulence proteins per se, but rather they may suppress responses of the plant that are important for pathogenicity to proceed (Jakobek et al., 1993). These

responses may be defense responses or other more general processes that maintain the status quo within the plant (e.g., the cell cycle).

Example 7 - Molecular Interactions of HopPsyA

HopPsyA interacts with the *Arabidopsis* Mad2 protein in the yeast 2-hybrid system. To determine a pathogenic target for HopPsyA, the yeast 2-hybrid system was used with cDNA libraries made from *Arabidopsis* (Fields and Song, 1989; Finley and Brent, 1994). In the yeast 2-hybrid system, a fusion between the protein of interest (the "bait") and the LexA DNA-binding domain was transformed into a yeast tester strain. A cDNA expression library was constructed in a vector that creates fusions to a transcriptional activator domain. This library was transformed into the tester strain en masse, and clones encoding partners for the "bait" are selected via their ability to bring the transcriptional activator domain into proximity with the DNA binding domain, thus initiating transcription of the *LEU2* selectable marker gene. A second round screening of candidates, that activate the *LEU2* marker, relies on their ability to also activate a *lacZ* reporter gene. Bait constructs were initially made witb *hopPsyA* in the yeast vector pEG202 that corresponded to a full-length HopPsyA-LexA fusion, the carboxy-terminal half of HopPsyA fused to LexA, and the amino-terminal half of HopPsyA fused to LexA, and named these constructs pLV23, pLV24, and pLV25, respectively. However, pLV23 was lethal to yeast and pLV25 activated the *lacZ* reporter gene in relatively high amounts on its own (i.e., without the activation domain present). Thus, both pLV23 and pLV25 were not used to screen for protein interactors via the yeast 2-hybrid system. pLV24, which contains the 3' portion of *hopPsyA* fused to *lexA,* proved to be an appropriate construct to use for bait in the yeast 2-hybrid system, because it did not autoactivate the *lacZ* reporter gene and, based on the *lacZ* repression assay using pJK101, the 'HopPsyA-LexA fusion produced by pLV24 appeared to localize to the nucleus. In addition, it was confirmed that pLV24 made a protein of the appropriate size that corresponds to HopPsyA by performing immunoblots with anti-HopPsyA antibodies on yeast cultures carrying this vector.

Initial screens with pLV24 and *Arabidopsis* cDNA libraries in the yeast 2-hybrid vector pJG4-5. From three independent screens, several hundred

putative interactors with HopPsyA were identified, each activating the two reporter systems to varying degrees. When these putative positive yeast strains were rescreened and criteria were limited to interactors that strongly induced both the *lacZ* reporter and *LEU2* gene in the presence of galactose, about 50 yeast strains were identified that appeared to contain pJG4-5 derivatives that encoded proteins that could interact with the C-terminal half of HopPsyA. DNA gel blots using PCR-amplified inserts from selected pJG4-5 derivatives as probes allowed each of these putative positives to be grouped. Approximately 50% of the pJG4-5 derivatives that encoded strong HopPsyA interactors belonged to the same group. A pJG4-5 derivative containing this insert, pLV116 was sequenced. The predicted amino acid sequence of the insert contained within pLV116 shared high amino acid identity to Mad2 homologs (for mitotic arrest deficient) found in yeast, humans, frogs, and corn. Moreover, based on amino acid comparison with the other Mad2 proteins, pLV116 contains a cDNA insert that corresponds to the full-length *mad2* mRNA. Table 2 below shows the amino acid percent identity of all of the Mad2 homologs currently in the databases.

Table 2: Percent Amino Acid Sequence Identity Between Different Mad2 Homologs*

Mad2 Homolog	*Arabidopsis*	Corn	Human	Mouse	Frog	Fission Yeast	Budding Yeast
Arabidopsis	-----						
Corn	81.3	-----					
Human	44.4	44.9	-----				
Mouse	45.4	45.9	94.6	-----			
Frog	43.3	42.9	78.3	77.3	-----		
Fission Yeast	40.4	41.9	43.8	43.8	46.3	-----	
Budding Yeast	38.3	38.8	39.3	39.3	39.8	45.4	-----

* Comparisons were made with the MEGALIGN program at DNAStar (Madison, WI) using sequences present in Genbank. Abbreviations and accession numbers are as follows: *Arabidopsis*, *A. thaliana* Col-0 (this work); Corn, *Zea mays* (AAD30555); Human, *Homo sapiens* (NP_002349); Mouse, *Mus musculus* (AAD09238); Frog, *Xenopus laevis*, (AAB41527); Fission yeast, *Schizosaccharomyces pombe* (AAB68597); Budding yeast, *Saccharamoyces cerevisiae* (P40958).

Not unexpectedly, the sequence of the *Arabidopsis* Mad2 protein is more closely related to the corn Mad2, the only plant Mad2 homolog represented in the databases. The corn Mad2 is about 82% identical to the *Arabidopsis* Mad2. Figures 16A-B show yeast strains containing either pLV24 and pJG4-5, pEG202 and pLV116, or pLV24

and pLV116 on leucine drop-out plates and plates containing X-Gal, showing that only when both HopPsyA and Mad2 are present, β-galactosidase and *LEU2* activity are induced. It is important to note that the cDNA library that yielded *mad2* has been used for many different yeast 2-hybrid screens and a *mad2* clone has never been isolated from it before. Thus, the results shown in Figures 16A-B are unlikely to represent an artifact produced by the nature of the cDNA library. Moreover, different Mad2 homologs are known to interact with specific proteins and one of these homologs was isolated with a yeast 2-hybrid screen using a protein of the spindle checkpoint as bait (Kim et al., 1998). This is reassuring for two reasons. First, other Mad2 homologs do not appear to be nonspecifically "sticky" proteins. Second, they appear to modulate cellular processes through protein-protein interactions.

The above results are very promising, because Mad2 is a regulator controlling the transition from metaphase to anaphase during mitosis, a key step in the cell cycle of eukaryotes. The eukaryotic cell cycle is dependent on the completion of earlier events before another phase of the cell cycle can be initiated. For example, before mitosis can occur DNA replication has to be completed. Some of these dependencies in the cell cycle can be relieved by mutations and represent checkpoints that insure the cell cycle is proceeding normally (Hartwell and Weinert, 1989). In pioneering work, Hoyt et al. and Li and Murray independently discovered that there is a checkpoint in place in *Saccharomyces cerevisiae* to monitor whether the spindle assembly required for chromosome segregation is completed (Hoyt et al., 1991; Li and Murray, 1991). This so-called spindle checkpoint was discovered when the observation was made that wild-type yeast cells plated onto media containing drugs that disrupt microtubule polymerization arrested in mitosis, whereas certain mutants proceeded into anaphase. These initial reports identified 6 different nonessential genes that are involved in the spindle checkpoint: *bub*1-3 named for budding uninhibited by benzimidazole and *mad*1-3 for mitotic arrest deficient. Mutations in these genes ignore spindle assembly abnormalities and attempt mitosis regardless. In the years since, the spindle checkpoint has been shown to be conserved in other eukaryotes and many advances have occurred resulting in a better picture of what is taking place at the spindle checkpoint (Glotzer, 1996; Rudner and Murray, 1996).

Required for the transition from metaphase to anaphase (as well as other cell cycle transitions) is the ubiquitin proteolysis pathway. Proteins that inhibit entry into anaphase (e.g., Pds1 in *S. cerevisiae*) are tagged for degradation via the ubiquitin pathway by the anaphase-promoting complex (APC) (King et al., 1996). Only when these proteins are degraded by the 26S proteosome are the cells allowed to cycle to anaphase. Although it is not well understood how the APC knows when to tag the anaphase inhibitors for degradation, there have been several important advances (Elledge, 1996; Elledge, 1998; Hardwick, 1998). The Mad2 protein and the Bub1 protein kinase have been shown to bind to kinetochores when these regions are not attached to microtubules (Chen et al., 1996; Li and Benezra, 1996; Taylor and McKeon, 1997; Yu et al., 1999). Thus, these proteins appear to somehow relay a signal that all of the chromosomes are not bound to spindle fibers ready to separate. Mad1 encodes a phosphoprotein, which becomes hyperphosphorylated when the spindle checkpoint is activated and the hyperphosphorylation of Mad1 is dependent on functional Bub1, Bub3, and Mad2 proteins (Hardwick and Murray, 1995). Another required protein in this checkpoint is Mps1, a protein kinase that activates the spindle checkpoint when overexpressed in a manner that is dependent on all of the Bub and Mad proteins, indicating that Mps1 acts very early in the spindle checkpoint (Hardwick et al., 1996).

Based on data from the different Mad2 homologs that have been studied, Mad2 appears to have a central role in the spindle checkpoint. Addition of Mad2 to *Xenopus* egg extracts results in inhibition of cyclin B degradation and mitotic arrest due to the inhibition of the ubiquitin ligase activity of the APC (Li et al., 1997). The overexpression of Mad2 from fission yeast causes mitotic arrest by activating the spindle checkpoint (He et al., 1997). Whereas, introducing anti-Mad2 antibodies into mammalian cell cultures causes early transition to anaphase in the absence of microtubule drugs, indicating that Mad2 is involved in the normal cell cycle. Several reports suggest that different Mad2 homologs directly interact with the APC (Li et al., 1997; Fang et al., 1998; Kallio et al., 1998). Another protein called Cdc20 in *S. cerevisiae* binds to the APC, is required for activation of the APC during certain cell cycles, and Mad2 binds to it (Hwang et al., 1998; Kim et al., 1998; Lorca et al., 1998; Wassmann and Benezra, 1998). The picture that is emerging from all of these exciting

findings is that Mad2 acts as an inhibitor of the APC, probably by binding to Cdc20. When Mad2 is not present, the Cdc20 binds to the APC, which activates the APC to degrade inhibitors of the transition to anaphase. Figure 12 shows a summary of the spindle checkpoint focusing on Mad2's involvement and using the names of the spindle checkpoint proteins from *S. cerevisiae*.

The plant spindle checkpoint: A possible target of bacterial pathogens. Many of the cell cycle proteins from animals have homologs in plants (Mironov et al., 1999). In fact, one of the early clues that there existed a spindle checkpoint was first made in plants. The observation noted was that chromosomes that lagged behind in their attachment to the spindle caused a delay in the transition to anaphase (Bajer and Mole-Bajer, 1956). Moreover, *mad2* has been recently isolated from corn and the Mad2 protein localization in plant cells undergoing mitosis is consistent with the localization of Mad2 in other systems (Yu et al., 1999). Based on a published meeting report, genes that encode components of the APC from *Arabidopsis* have been recently cloned (Inze et al., 1999). Thus, it appears that a functional spindle checkpoint probably is conserved in plants. The data presented above shows that the *P. syringae* HopPsyA protein interacts with the *Arabidopsis* Mad2 protein in the yeast 2-hybrid system.

It is possible that a pathogenic strategy of a bacterial plant pathogen is to alter the plant cell cycle. Duan et al. recently reported that *pthA*, a member of the *avrBs3* family of *avr* genes from *X. citri,* is expressed in citrus and causes cell enlargement and cell division, which may implicate the plant cell cycle (Duan et al., 1999). If HopPsyA does target Mad2, at least two possible benefits to pathogenicity can be envisioned. Since plant cells in mature leaves are quiescent, one benefit of delivering HopPsyA into these cells may be that it may trigger cell division through its interaction with Mad2. This is consistent with the observation that anti-Mad2 antibodies cause an early onset of anaphase in mammalian cells (Gorbsky et al., 1998). More plant cells near the pathogen may increase the nutrients available in the apoplast. A second possible benefit may occur if HopPsyA is delivered into plant cells actively dividing in young leaves. Delivery of HopPsyA into plant cells of these leaves may derail the spindle checkpoint through its interaction with Mad2. These cells would be prone to more mistakes segregating their chromosomes; in some cells

this would result in death and the cellular contents would ultimately leak into the apoplast providing nutrients for the pathogen.

Example 8 - Cytotoxic Effects of HopPtoA and HopPsyA Expressed in Yeast

Both *hopPtoA* (SEQ. ID. No. 6) and *hopPsyA* (SEQ. ID. No. 35) were first cloned into pFLAG-CTC (Kodak) to generate an in-frame fusion with the FLAG epitope, which permitted monitoring of protein production with anti-FLAG monoclonal antibodies. The FLAG-tagged genes were then cloned under the control of the GAL1 promoter in the yeast shuttle vector p415GAL1 (Mumberg et al., 1994). These regulatable promoters of *Saccharomyces cerevisiae* allowed comparison of transcriptional activity and heterologous expression. The recombinant plasmids were transformed into uracil auxotrophic yeast strains FY833/4, selecting for growth on SC-Ura (synthetic complete medium lacking uracil) based on the presence of the URA3 gene on the plasmid. The transformants were then streaked onto SC-Ura medium plates containing either 2% galactose (which will induce expression of HopPsyA and HopPtoA) or 2% glucose. No growth was observed on the plates supplemented with 2% galactose. This effect was observed with repeated testing and was not observed with empty vector controls, with four other effectors similarly cloned into p415GAL1, or when raffinose was used instead of galactose. FLAG-tagged nontoxic Avr proteins were used to confirm that the genes were differentially expressed, as expected, on plates containing galactose. Importantly, the toxic effect with HopPsyA was observed when the encoding gene was recloned into p416GALS, which expresses foreign genes at a substantially lower level than p415GAL1.

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Each of the references cited herein or otherwise listed below are expressly incorporated by reference in their entirety into this specification.

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Although the invention has been described in detail for the purposes of illustration, it is understood that such detail is solely for that purpose, and variations can be made therein by those skilled in the art without departing from the spirit and scope of the invention which is defined by the following claims.